

Erich Grotewold

List of Publications by Year in descending order

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Version: 2024-02-01

164
papers

21,327
citations

20036

63
h-index

11608

140
g-index

200
all docs

200
docs citations

200
times ranked

23272
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2022, 34, 514-534.	3.1	30
2	Exploring <i>Camelina sativa</i> lipid metabolism regulation by combining gene co-expression and <sc>DNA</sc> affinity purification analyses. <i>Plant Journal</i> , 2022, 110, 589-606.	2.8	13
3	Cis-regulatory sequences in plants: Their importance, discovery, and future challenges. <i>Plant Cell</i> , 2022, 34, 718-741.	3.1	125
4	Modeling temporal and hormonal regulation of plant transcriptional response to wounding. <i>Plant Cell</i> , 2022, 34, 867-888.	3.1	22
5	Microautophagy Mediates Vacuolar Delivery of Storage Proteins in Maize Aleurone Cells. <i>Frontiers in Plant Science</i> , 2022, 13, 833612.	1.7	11
6	Natural variation and improved genome annotation of the emerging biofuel crop field pennycress (<i>Thlaspi arvense</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	5
7	Normalizing and Correcting Variable and Complex LC-MS Metabolomic Data with the R Package pseudoDrift. <i>Metabolites</i> , 2022, 12, 435.	1.3	1
8	Rhamnose in plants - from biosynthesis to diverse functions. <i>Plant Science</i> , 2021, 302, 110687.	1.7	41
9	A hydrophobic residue stabilizes dimers of regulatory ACT-like domains in plant basic helix-loop-helix transcription factors. <i>Journal of Biological Chemistry</i> , 2021, 296, 100708.	1.6	9
10	Discovery of modules involved in the biosynthesis and regulation of maize phenolic compounds. <i>Plant Science</i> , 2020, 291, 110364.	1.7	11
11	Diversity of genetic lesions characterizes new <i>Arabidopsis</i> flavonoid pigment mutant alleles from T-DNA collections. <i>Plant Science</i> , 2020, 291, 110335.	1.7	10
12	CamRegBase: a gene regulation database for the biofuel crop, <i>Camelina sativa</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	7
13	Synergy between the anthocyanin and RDR6/SGS3/DCL4 siRNA pathways expose hidden features of <i>Arabidopsis</i> carbon metabolism. <i>Nature Communications</i> , 2020, 11, 2456.	5.8	17
14	Plant specialized metabolism. <i>Plant Science</i> , 2020, 298, 110579.	1.7	25
15	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	3.1	60
16	Challenges of Translating Gene Regulatory Information into Agronomic Improvements. <i>Trends in Plant Science</i> , 2019, 24, 1075-1082.	4.3	34
17	<i>Arabidopsis</i> EMSY-like (EML) histone readers are necessary for post-fertilization seed development, but prevent fertilization-independent seed formation. <i>Plant Science</i> , 2019, 285, 99-109.	1.7	10
18	<i>Arabidopsis</i> JMJD5/JMJ30 Acts Independently of LUX ARRHYTHMO Within the Plant Circadian Clock to Enable Temperature Compensation. <i>Frontiers in Plant Science</i> , 2019, 10, 57.	1.7	19

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19	Apigenin produced by maize flavone synthase I and II protects plants against UV-B-induced damage. <i>Plant, Cell and Environment</i> , 2019, 42, 495-508.	2.8	54
20	Beyond the wall: High-throughput quantification of plant soluble and cell-wall bound phenolics by liquid chromatography tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2019, 1589, 93-104.	1.8	32
21	Tomato floral induction and flower development are orchestrated by the interplay between gibberellin and two unrelated microRNA-controlled modules. <i>New Phytologist</i> , 2019, 221, 1328-1344.	3.5	61
22	Arabidopsis MATE 45 antagonizes local abscisic acid signaling to mediate development and abiotic stress responses. <i>Plant Direct</i> , 2018, 2, e00087.	0.8	8
23	Topological and statistical analyses of gene regulatory networks reveal unifying yet quantitatively different emergent properties. <i>PLoS Computational Biology</i> , 2018, 14, e1006098.	1.5	48
24	Following Phenotypes: An Exploration of Mendelian Genetics Using Arabidopsis Plants. <i>American Biology Teacher</i> , 2018, 80, 291-300.	0.1	6
25	Imaging Vacuolar Anthocyanins with Fluorescence Lifetime Microscopy (FLIM). <i>Methods in Molecular Biology</i> , 2018, 1789, 131-141.	0.4	3
26	Genome-Wide TSS Identification in Maize. <i>Methods in Molecular Biology</i> , 2018, 1830, 239-256.	0.4	1
27	Challenges and opportunities for improving food quality and nutrition through plant biotechnology. <i>Current Opinion in Biotechnology</i> , 2017, 44, 124-129.	3.3	34
28	Identification of biochemical features of defective <i>Coffea arabica</i> L. beans. <i>Food Research International</i> , 2017, 95, 59-67.	2.9	20
29	Design of Knowledge Bases for Plant Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2017, 1629, 207-223.	0.4	1
30	WIND1 Promotes Shoot Regeneration through Transcriptional Activation of <i>ENHANCER OF SHOOT REGENERATION1</i> in Arabidopsis. <i>Plant Cell</i> , 2017, 29, 54-69.	3.1	164
31	Standardized Method for High-throughput Sterilization of Arabidopsis Seeds. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	69
32	The BIF Domain in Plant bHLH Proteins Is an ACT-Like Domain. <i>Plant Cell</i> , 2017, 29, 1800-1802.	3.1	12
33	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	2.3	11
34	News from the plant world: Listening to transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1-2.	0.9	8
35	Combinatorial control of plant gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 31-40.	0.9	44
36	A Maize Gene Regulatory Network for Phenolic Metabolism. <i>Molecular Plant</i> , 2017, 10, 498-515.	3.9	74

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37	The challenges faced by living stock collections in the USA. <i>ELife</i> , 2017, 6, .	2.8	7
38	Dietary Apigenin Exerts Immune-Regulatory Activity in Vivo by Reducing NF- κ B Activity, Halting Leukocyte Infiltration and Restoring Normal Metabolic Function. <i>International Journal of Molecular Sciences</i> , 2016, 17, 323.	1.8	69
39	Flavones: From Biosynthesis to Health Benefits. <i>Plants</i> , 2016, 5, 27.	1.6	209
40	Identification and Characterization of Maize <i>salmon silks</i> Genes Involved in Insecticidal Maysin Biosynthesis. <i>Plant Cell</i> , 2016, 28, 1297-1309.	3.1	64
41	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	3.5	186
42	Establishing the Architecture of Plant Gene Regulatory Networks. <i>Methods in Enzymology</i> , 2016, 576, 251-304.	0.4	8
43	Using fluorescence lifetime microscopy to study the subcellular localization of anthocyanins. <i>Plant Journal</i> , 2016, 88, 895-903.	2.8	19
44	MYB31/MYB42 Syntelogs Exhibit Divergent Regulation of Phenylpropanoid Genes in Maize, Sorghum and Rice. <i>Scientific Reports</i> , 2016, 6, 28502.	1.6	81
45	Flavonols drive plant microevolution. <i>Nature Genetics</i> , 2016, 48, 112-113.	9.4	9
46	Core Promoter Plasticity Between Maize Tissues and Genotypes Contrasts with Predominance of Sharp Transcription Initiation Sites. <i>Plant Cell</i> , 2015, 27, 3309-3320.	3.1	65
47	A MYB/ZML Complex Regulates Wound-Induced Lignin Genes in Maize. <i>Plant Cell</i> , 2015, 27, 3245-3259.	3.1	104
48	A coherent transcriptional feed-forward motif model for mediating auxin-sensitive PIN3 expression during lateral root development. <i>Nature Communications</i> , 2015, 6, 8821.	5.8	70
49	Abiotic stresses induce different localizations of anthocyanins in Arabidopsis. <i>Plant Signaling and Behavior</i> , 2015, 10, e1027850.	1.2	118
50	Important biological information uncovered in previously unaligned reads from chromatin immunoprecipitation experiments (ChIP-Seq). <i>Scientific Reports</i> , 2015, 5, 8635.	1.6	5
51	The Identification of Maize and Arabidopsis Type I FLAVONE SYNTHASEs Links Flavones with Hormones and Biotic Interactions. <i>Plant Physiology</i> , 2015, 169, 1090-1107.	2.3	87
52	Anthocyanin Vacuolar Inclusions Form by a Microautophagy Mechanism. <i>Plant Cell</i> , 2015, 27, 2545-2559.	3.1	153
53	Transcriptional regulation of PIN genes by FOUR LIPS and MYB88 during Arabidopsis root gravitropism. <i>Nature Communications</i> , 2015, 6, 8822.	5.8	74
54	Metabolic engineering to enhance the value of plants as green factories. <i>Metabolic Engineering</i> , 2015, 27, 83-91.	3.6	65

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55	Protocol for the Generation of a Transcription Factor Open Reading Frame Collection (TFome). Bio-protocol, 2015, 5, .	0.2	3
56	Flavone-rich maize: an opportunity to improve the nutritional value of an important commodity crop. Frontiers in Plant Science, 2014, 5, 440.	1.7	54
57	The Maize <sc>TF</sc>ome â€œ development of a transcription factor open reading frame collection for functional genomics. Plant Journal, 2014, 80, 356-366.	2.8	55
58	Not all anthocyanins are born equal: distinct patterns induced by stress in Arabidopsis. Planta, 2014, 240, 931-940.	1.6	129
59	Regulatory modules controlling maize inflorescence architecture. Genome Research, 2014, 24, 431-443.	2.4	160
60	Helixâ€loopâ€helix/basic helixâ€loopâ€helix transcription factor network represses cell elongation in <i>Arabidopsis</i> through an apparent incoherent feed-forward loop. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2824-2829.	3.3	76
61	Handling Arabidopsis Plants: Growth, Preservation of Seeds, Transformation, and Genetic Crosses. Methods in Molecular Biology, 2014, 1062, 3-25.	0.4	54
62	Arabidopsis Database and Stock Resources. Methods in Molecular Biology, 2014, 1062, 65-96.	0.4	10
63	Turning over a new leaf in plant genomics. Genome Biology, 2013, 14, 403.	3.8	4
64	A chemical complementation approach reveals genes and interactions of flavonoids with other pathways. Plant Journal, 2013, 74, 383-397.	2.8	74
65	Flavonols Protect Arabidopsis Plants against UV-B Deleterious Effects. Molecular Plant, 2013, 6, 1376-1379.	3.9	74
66	Highâ€resolution computational imaging of leaf hair patterning using polarized light microscopy. Plant Journal, 2013, 73, 701-708.	2.8	17
67	Molecular basis for the action of a dietary flavonoid revealed by the comprehensive identification of apigenin human targets. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2153-62.	3.3	115
68	Identification of a Bifunctional Maize C- and O-Glucosyltransferase. Journal of Biological Chemistry, 2013, 288, 31678-31688.	1.6	122
69	Evolution and Expression of Tandem Duplicated Maize Flavonol Synthase Genes. Frontiers in Plant Science, 2012, 3, 101.	1.7	36
70	A Genome-Wide Regulatory Framework Identifies Maize <i>Pericarp Color1</i> Controlled Genes. Plant Cell, 2012, 24, 2745-2764.	3.1	148
71	Transcriptional repression of the APC/C activator CCS52A1 promotes active termination of cell growth. EMBO Journal, 2012, 31, 4488-4501.	3.5	60
72	Regulatory switch enforced by basic helix-loop-helix and ACT-domain mediated dimerizations of the maize transcription factor R. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2091-7.	3.3	92

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73	Grass phenylpropanoids: Regulate before using!. <i>Plant Science</i> , 2012, 184, 112-120.	1.7	79
74	From plant gene regulatory grids to network dynamics. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 454-465.	0.9	41
75	Expression of flavonoid 3- <i>OH</i> -hydroxylase is controlled by P1, the regulator of 3-deoxyflavonoid biosynthesis in maize. <i>BMC Plant Biology</i> , 2012, 12, 196.	1.6	65
76	Analysis of the P1 promoter in response to UV-B radiation in allelic variants of high-altitude maize. <i>BMC Plant Biology</i> , 2012, 12, 92.	1.6	14
77	Apigenin induces DNA damage through the PKC δ -dependent activation of ATM and H2AX causing down-regulation of genes involved in cell cycle control and DNA repair. <i>Biochemical Pharmacology</i> , 2012, 84, 1571-1580.	2.0	46
78	Unraveling the KNOTTED1 regulatory network in maize meristems. <i>Genes and Development</i> , 2012, 26, 1685-1690.	2.7	258
79	Identification of Human α -Flavonoid Targets Using an Innovative Approach Reveals New Mechanisms Involved in Their Anti-inflammatory Activities. <i>FASEB Journal</i> , 2012, 26, 251.5.	0.2	0
80	Developmental regulation of CYCA2s contributes to tissue-specific proliferation in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2011, 30, 3430-3441.	3.5	113
81	SELEX (Systematic Evolution of Ligands by EXponential Enrichment), as a Powerful Tool for Deciphering the Protein-DNA Interaction Space. <i>Methods in Molecular Biology</i> , 2011, 754, 249-258.	0.4	38
82	Evolutionary and comparative analysis of MYB and bHLH plant transcription factors. <i>Plant Journal</i> , 2011, 66, 94-116.	2.8	1,014
83	Source verification of misidentified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011, 67, 554-566.	2.8	63
84	Interplay of MYB factors in differential cell expansion, and consequences for tomato fruit development. <i>Plant Journal</i> , 2011, 68, 337-350.	2.8	55
85	Brachypodium as a Model for the Grasses: Today and the Future \hat{A} . <i>Plant Physiology</i> , 2011, 157, 3-13.	2.3	243
86	AGRIS: the Arabidopsis Gene Regulatory Information Server, an update. <i>Nucleic Acids Research</i> , 2011, 39, D1118-D1122.	6.5	289
87	POPCorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-10.	2.2	20
88	Emergence of Switch-Like Behavior in a Large Family of Simple Biochemical Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1002039.	1.5	41
89	Encyclopedias of DNA Elements for Plant Genomes. <i>Science, Engineering, and Biology Informatics</i> , 2011, , 159-178.	0.1	1
90	Transcription Factors, Gene Regulatory Networks and Agronomic Traits. <i>Advances in Agroecology</i> , 2011, , 65-94.	0.3	1

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91	Cloning and characterization of a UV-B-inducible maize flavonol synthase. <i>Plant Journal</i> , 2010, 62, 77-91.	2.8	126
92	ZmMYB31 directly represses maize lignin genes and redirects the phenylpropanoid metabolic flux. <i>Plant Journal</i> , 2010, 64, 633-644.	2.8	245
93	Role of the stomatal development regulators FLP/MYB88 in abiotic stress responses. <i>Plant Journal</i> , 2010, 64, 731-739.	2.8	104
94	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
95	The Formation of Anthocyanic Vacuolar Inclusions in <i>Arabidopsis thaliana</i> and Implications for the Sequestration of Anthocyanin Pigments. <i>Molecular Plant</i> , 2010, 3, 78-90.	3.9	134
96	Regulation of Cell Proliferation in the Stomatal Lineage by the <i>Arabidopsis</i> MYB FOUR LIPS via Direct Targeting of Core Cell Cycle Genes. <i>Plant Cell</i> , 2010, 22, 2306-2321.	3.1	152
97	MYB transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2010, 15, 573-581.	4.3	2,987
98	Components and Mechanisms of Regulation of Gene Expression. <i>Methods in Molecular Biology</i> , 2010, 674, 23-32.	0.4	15
99	Construction of Genomic Regulatory Encyclopedias: Strategies and Case Studies. , 2009, , .		0
100	Discovery of Regulatory Networks in Plants by Linking Promoter and Transcription Factor Databases. , 2009, , .		0
101	A Recommendation for Naming Transcription Factor Proteins in the Grasses. <i>Plant Physiology</i> , 2009, 149, 4-6.	2.3	45
102	A Systems Approach Reveals Regulatory Circuitry for <i>Arabidopsis</i> Trichome Initiation by the GL3 and GL1 Selectors. <i>PLoS Genetics</i> , 2009, 5, e1000396.	1.5	185
103	GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses. <i>Plant Physiology</i> , 2009, 149, 171-180.	2.3	260
104	The word landscape of the non-coding segments of the <i>Arabidopsis thaliana</i> genome. <i>BMC Genomics</i> , 2009, 10, 463.	1.2	28
105	The capacity for multistability in small gene regulatory networks. <i>BMC Systems Biology</i> , 2009, 3, 96.	3.0	33
106	Maize Transcription Factors. , 2009, , 693-713.		3
107	Participation of Phytochemicals in Plant Development and Growth. , 2009, , 269-279.		6
108	Gene-Specific and Genome-Wide CHIP Approaches to Study Plant Transcriptional Networks. <i>Methods in Molecular Biology</i> , 2009, 553, 3-12.	0.4	25

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109	Transcription factors for predictive plant metabolic engineering: are we there yet?. <i>Current Opinion in Biotechnology</i> , 2008, 19, 138-144.	3.3	146
110	Plant biotechnology – Predictive, green and quantitative. <i>Current Opinion in Biotechnology</i> , 2008, 19, 129-130.	3.3	4
111	Serial ChIP as a tool to investigate the co-localization or exclusion of proteins on plant genes. <i>Plant Methods</i> , 2008, 4, 25.	1.9	14
112	The TTG1-bHLH-MYB complex controls trichome cell fate and patterning through direct targeting of regulatory loci. <i>Development (Cambridge)</i> , 2008, 135, 1991-1999.	1.2	311
113	Trafficking and Sequestration of Anthocyanins. <i>Natural Product Communications</i> , 2008, 3, 1934578X0800300.	0.2	33
114	Apigenin Blocks Lipopolysaccharide-Induced Lethality In Vivo and Proinflammatory Cytokines Expression by Inactivating NF- κ B through the Suppression of p65 Phosphorylation. <i>Journal of Immunology</i> , 2007, 179, 7121-7127.	0.4	301
115	The basic helix–loop–helix domain of maize R links transcriptional regulation and histone modifications by recruitment of an EMSY-related factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17222-17227.	3.3	82
116	Participation of the Arabidopsis bHLH Factor GL3 in Trichome Initiation Regulatory Events. <i>Plant Physiology</i> , 2007, 145, 736-746.	2.3	181
117	A Trafficking Pathway for Anthocyanins Overlaps with the Endoplasmic Reticulum-to-Vacuole Protein-Sorting Route in Arabidopsis and Contributes to the Formation of Vacuolar Inclusions. <i>Plant Physiology</i> , 2007, 145, 1323-1335.	2.3	189
118	Inhibition of AtMYB2 DNA-binding by nitric oxide involves cysteine S-nitrosylation. <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 1048-1053.	1.0	133
119	Characterization of Anthocyanidin Synthase (ANS) Gene and anthocyanidin in rare medicinal plant-Saussurea medusa. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 89, 63-73.	1.2	20
120	Expression and Molecular Characterization of ZmMYB-IF35 and Related R2R3-MYB Transcription Factors. <i>Molecular Biotechnology</i> , 2007, 37, 155-164.	1.3	16
121	THE GENETICS AND BIOCHEMISTRY OF FLORAL PIGMENTS. <i>Annual Review of Plant Biology</i> , 2006, 57, 761-780.	8.6	1,233
122	Apigenin-induced-apoptosis is mediated by the activation of PKC ζ and caspases in leukemia cells. <i>Biochemical Pharmacology</i> , 2006, 72, 681-692.	2.0	144
123	AGRIS and AtRegNet. A Platform to Link cis-Regulatory Elements and Transcription Factors into Regulatory Networks. <i>Plant Physiology</i> , 2006, 140, 818-829.	2.3	249
124	An ACT-like Domain Participates in the Dimerization of Several Plant Basic-helix-loop-helix Transcription Factors. <i>Journal of Biological Chemistry</i> , 2006, 281, 28964-28974.	1.6	124
125	Flavonoids as developmental regulators. <i>Current Opinion in Plant Biology</i> , 2005, 8, 317-323.	3.5	514
126	Genome wide analysis of Arabidopsis core promoters. <i>BMC Genomics</i> , 2005, 6, 25.	1.2	180

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127	Light-induced morphological alteration in anthocyanin-accumulating vacuoles of maize cells. BMC Plant Biology, 2005, 5, 7.	1.6	58
128	The tomato early fruit specific gene Lefsm1 defines a novel class of plant-specific SANT/MYB domain proteins. Planta, 2005, 221, 197-211.	1.6	40
129	Covalent attachment of the plant natural product naringenin to small glass and ceramic beads. BMC Chemical Biology, 2005, 5, 3.	1.6	6
130	Cloning and characterization of a flavanone 3-hydroxylase gene from <i>Saussurea medusa</i> . DNA Sequence, 2005, 16, 121-129.	0.7	14
131	Plant metabolic diversity: a regulatory perspective. Trends in Plant Science, 2005, 10, 57-62.	4.3	144
132	Two Cysteines in Plant R2R3 MYB Domains Participate in REDOX-dependent DNA Binding. Journal of Biological Chemistry, 2004, 279, 37878-37885.	1.6	92
133	Different Mechanisms Participate in the R-dependent Activity of the R2R3 MYB Transcription Factor C1. Journal of Biological Chemistry, 2004, 279, 48205-48213.	1.6	123
134	Comparison of ESTs from juvenile and adult phases of the giant unicellular green alga <i>Acetabularia acetabulum</i> . BMC Plant Biology, 2004, 4, 3.	1.6	25
135	The challenges of moving chemicals within and out of cells: insights into the transport of plant natural products. Planta, 2004, 219, 906-9.	1.6	96
136	RNase P as a tool for disruption of gene expression in maize cells. Biochemical Journal, 2004, 380, 611-616.	1.7	13
137	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. BMC Bioinformatics, 2003, 4, 25.	1.2	349
138	Sub-cellular trafficking of phytochemicals explored using auto-fluorescent compounds in maize cells. BMC Plant Biology, 2003, 3, 10.	1.6	35
139	Manipulating the accumulation of phenolics in maize cultured cells using transcription factors. Biochemical Engineering Journal, 2003, 14, 207-216.	1.8	30
140	Root Exudation and Rhizosphere Biology. Plant Physiology, 2003, 132, 44-51.	2.3	1,216
141	Metabolite Profiling as a Functional Genomics Tool. , 2003, 236, 415-426.		6
142	Recently Duplicated Maize R2R3 Myb Genes Provide Evidence for Distinct Mechanisms of Evolutionary Divergence after Duplication. Plant Physiology, 2003, 131, 610-620.	2.3	151
143	Chapter three Regulation of anthocyanin pigmentation. Recent Advances in Phytochemistry, 2003, 37, 59-78.	0.5	29
144	Transposon Insertions in the Promoter of the <i>Zea mays a1</i> Gene Differentially Affect Transcription by the Myb Factors P and C1. Genetics, 2002, 161, 793-801.	1.2	43

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145	Fungal Zuotin Proteins Evolved from MIDA1-like Factors by Lineage-Specific Loss of MYB Domains. <i>Molecular Biology and Evolution</i> , 2001, 18, 1401-1412.	3.5	26
146	Functional Conservation of Plant Secondary Metabolic Enzymes Revealed by Complementation of Arabidopsis Flavonoid Mutants with Maize Genes. <i>Plant Physiology</i> , 2001, 127, 46-57.	2.3	93
147	Chapter Five Transcription factors and metabolic engineering: Novel applications for ancient tools. <i>Recent Advances in Phytochemistry</i> , 2001, 35, 79-109.	0.5	14
148	A novel reverse-genetic approach (SIMF) identifies Mutator insertions in new Myb genes. <i>Planta</i> , 2000, 211, 887-893.	1.6	3
149	Identification of the residues in the Myb domain of maize C1 that specify the interaction with the bHLH cofactor R. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13579-13584.	3.3	292
150	Newly Discovered Plant c-myb-Like Genes Rewrite the Evolution of the Plant myb Gene Family : Fig. 1.. <i>Plant Physiology</i> , 1999, 121, 21-24.	2.3	79
151	Maize R2R3 Myb Genes: Sequence Analysis Reveals Amplification in the Higher Plants. <i>Genetics</i> , 1999, 153, 427-444.	1.2	150
152	How genes paint flowers and seeds. <i>Trends in Plant Science</i> , 1998, 3, 212-217.	4.3	804
153	Essential Dynamics from NMR Clusters: Dynamic Properties of the Myb DNA-Binding Domain and a Hinge-Bending Enhancing Variant. <i>Methods</i> , 1998, 14, 318-328.	1.9	30
154	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. <i>Plant Cell</i> , 1998, 10, 721-740.	3.1	343
155	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. <i>Plant Cell</i> , 1998, 10, 721.	3.1	11
156	Differences between Plant and Animal Myb Domains Are Fundamental for DNA Binding Activity, and Chimeric Myb Domains Have Novel DNA Binding Specificities. <i>Journal of Biological Chemistry</i> , 1997, 272, 563-571.	1.6	87
157	Evidence for Direct Activation of an Anthocyanin Promoter by the Maize C1 Protein and Comparison of DNA Binding by Related Myb Domain Proteins. <i>Plant Cell</i> , 1997, 9, 611.	3.1	32
158	Isolation and characterization of a maize gene encoding chalcone flavanone isomerase. <i>Molecular Genetics and Genomics</i> , 1994, 242, 1-8.	2.4	70
159	The myb-homologous P gene controls phlobaphene pigmentation in maize floral organs by directly activating a flavonoid biosynthetic gene subset. <i>Cell</i> , 1994, 76, 543-553.	13.5	644
160	The cDNA sequence and expression of an ubiquitin-tail gene fusion in <i>Neurospora crassa</i> . <i>Gene</i> , 1991, 102, 133-137.	1.0	11
161	A possible hot spot for Ac insertion in the maize P gene. <i>Molecular Genetics and Genomics</i> , 1991, 230, 329-331.	2.4	33
162	Ubiquitin expression in <i>Neurospora crassa</i> : cloning and sequencing of a polyubiquitin gene. <i>Nucleic Acids Research</i> , 1989, 17, 6153-6165.	6.5	24

#	ARTICLE	IF	CITATIONS
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