

Erich Grotewold

List of Publications by Year in descending order

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164
papers

21,327
citations

17440

63
h-index

10158

140
g-index

200
all docs

200
docs citations

200
times ranked

21088
citing authors

#	ARTICLE	IF	CITATIONS
1	MYB transcription factors in Arabidopsis. Trends in Plant Science, 2010, 15, 573-581.	8.8	2,987
2	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	27.8	1,685
3	THE GENETICS AND BIOCHEMISTRY OF FLORAL PIGMENTS. Annual Review of Plant Biology, 2006, 57, 761-780.	18.7	1,233
4	Root Exudation and Rhizosphere Biology. Plant Physiology, 2003, 132, 44-51.	4.8	1,216
5	Evolutionary and comparative analysis of MYB and bHLH plant transcription factors. Plant Journal, 2011, 66, 94-116.	5.7	1,014
6	How genes paint flowers and seeds. Trends in Plant Science, 1998, 3, 212-217.	8.8	804
7	The myb-homologous P gene controls phlobaphene pigmentation in maize floral organs by directly activating a flavonoid biosynthetic gene subset. Cell, 1994, 76, 543-553.	28.9	644
8	Flavonoids as developmental regulators. Current Opinion in Plant Biology, 2005, 8, 317-323.	7.1	514
9	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. BMC Bioinformatics, 2003, 4, 25.	2.6	349
10	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. Plant Cell, 1998, 10, 721-740.	6.6	343
11	The TTG1-bHLH-MYB complex controls trichome cell fate and patterning through direct targeting of regulatory loci. Development (Cambridge), 2008, 135, 1991-1999.	2.5	311
12	Apigenin Blocks Lipopolysaccharide-Induced Lethality In Vivo and Proinflammatory Cytokines Expression by Inactivating NF- κ B through the Suppression of p65 Phosphorylation. Journal of Immunology, 2007, 179, 7121-7127.	0.8	301
13	Identification of the residues in the Myb domain of maize C1 that specify the interaction with the bHLH cofactor R. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13579-13584.	7.1	292
14	AGRIS: the Arabidopsis Gene Regulatory Information Server, an update. Nucleic Acids Research, 2011, 39, D1118-D1122.	14.5	289
15	GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses \hat{A} \hat{A} . Plant Physiology, 2009, 149, 171-180.	4.8	260
16	Unraveling the KNOTTED1 regulatory network in maize meristems. Genes and Development, 2012, 26, 1685-1690.	5.9	258
17	AGRIS and AtRegNet. A Platform to Link cis-Regulatory Elements and Transcription Factors into Regulatory Networks. Plant Physiology, 2006, 140, 818-829.	4.8	249
18	ZmMYB31 directly represses maize lignin genes and redirects the phenylpropanoid metabolic flux. Plant Journal, 2010, 64, 633-644.	5.7	245

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19	Brachypodium as a Model for the Grasses: Today and the Future. <i>Plant Physiology</i> , 2011, 157, 3-13.	4.8	243
20	Flavones: From Biosynthesis to Health Benefits. <i>Plants</i> , 2016, 5, 27.	3.5	209
21	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.	4.8	189
22	50 Years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	7.3	186
23	A Systems Approach Reveals Regulatory Circuitry for Arabidopsis Trichome Initiation by the GL3 and GL1 Selectors. <i>PLoS Genetics</i> , 2009, 5, e1000396.	3.5	185
24	Participation of the Arabidopsis bHLH Factor GL3 in Trichome Initiation Regulatory Events. <i>Plant Physiology</i> , 2007, 145, 736-746.	4.8	181
25	Genome wide analysis of Arabidopsis core promoters. <i>BMC Genomics</i> , 2005, 6, 25.	2.8	180
26	WIND1 Promotes Shoot Regeneration through Transcriptional Activation of <i>ENHANCER OF SHOOT REGENERATION1</i> in Arabidopsis. <i>Plant Cell</i> , 2017, 29, 54-69.	6.6	164
27	Regulatory modules controlling maize inflorescence architecture. <i>Genome Research</i> , 2014, 24, 431-443.	5.5	160
28	Anthocyanin Vacuolar Inclusions Form by a Microautophagy Mechanism. <i>Plant Cell</i> , 2015, 27, 2545-2559.	6.6	153
29	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.	6.6	152
30	Recently Duplicated Maize R2R3 Myb Genes Provide Evidence for Distinct Mechanisms of Evolutionary Divergence after Duplication. <i>Plant Physiology</i> , 2003, 131, 610-620.	4.8	151
31	Maize R2R3 Myb Genes: Sequence Analysis Reveals Amplification in the Higher Plants. <i>Genetics</i> , 1999, 153, 427-444.	2.9	150
32	A Genome-Wide Regulatory Framework Identifies Maize <i>Pericarp Color1</i> Controlled Genes. <i>Plant Cell</i> , 2012, 24, 2745-2764.	6.6	148
33	Transcription factors for predictive plant metabolic engineering: are we there yet?. <i>Current Opinion in Biotechnology</i> , 2008, 19, 138-144.	6.6	146
34	Plant metabolic diversity: a regulatory perspective. <i>Trends in Plant Science</i> , 2005, 10, 57-62.	8.8	144
35	Apigenin-induced-apoptosis is mediated by the activation of PKC ζ and caspases in leukemia cells. <i>Biochemical Pharmacology</i> , 2006, 72, 681-692.	4.4	144
36	The Formation of Anthocyanic Vacuolar Inclusions in Arabidopsis thaliana and Implications for the Sequestration of Anthocyanin Pigments. <i>Molecular Plant</i> , 2010, 3, 78-90.	8.3	134

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37	Inhibition of AtMYB2 DNA-binding by nitric oxide involves cysteine S-nitrosylation. <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 1048-1053.	2.1	133
38	Not all anthocyanins are born equal: distinct patterns induced by stress in <i>Arabidopsis</i> . <i>Planta</i> , 2014, 240, 931-940.	3.2	129
39	Cloning and characterization of a UV-B-inducible maize flavonol synthase. <i>Plant Journal</i> , 2010, 62, 77-91.	5.7	126
40	Cis-regulatory sequences in plants: Their importance, discovery, and future challenges. <i>Plant Cell</i> , 2022, 34, 718-741.	6.6	125
41	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.	3.4	124
42	Different Mechanisms Participate in the R-dependent Activity of the R2R3 MYB Transcription Factor C1. <i>Journal of Biological Chemistry</i> , 2004, 279, 48205-48213.	3.4	123
43	Identification of a Bifunctional Maize C- and O-Glucosyltransferase. <i>Journal of Biological Chemistry</i> , 2013, 288, 31678-31688.	3.4	122
44	Abiotic stresses induce different localizations of anthocyanins in <i>Arabidopsis</i> . <i>Plant Signaling and Behavior</i> , 2015, 10, e1027850.	2.4	118
45	Molecular basis for the action of a dietary flavonoid revealed by the comprehensive identification of apigenin human targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2153-62.	7.1	115
46	Developmental regulation of CYCA2s contributes to tissue-specific proliferation in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2011, 30, 3430-3441.	7.8	113
47	Role of the stomatal development regulators FLP/MYB88 in abiotic stress responses. <i>Plant Journal</i> , 2010, 64, 731-739.	5.7	104
48	A MYB/ZML Complex Regulates Wound-Induced Lignin Genes in Maize. <i>Plant Cell</i> , 2015, 27, 3245-3259.	6.6	104
49	The challenges of moving chemicals within and out of cells: insights into the transport of plant natural products. <i>Planta</i> , 2004, 219, 906-9.	3.2	96
50	Functional Conservation of Plant Secondary Metabolic Enzymes Revealed by Complementation of <i>Arabidopsis</i> Flavonoid Mutants with Maize Genes. <i>Plant Physiology</i> , 2001, 127, 46-57.	4.8	93
51	Two Cysteines in Plant R2R3 MYB Domains Participate in REDOX-dependent DNA Binding. <i>Journal of Biological Chemistry</i> , 2004, 279, 37878-37885.	3.4	92
52	Regulatory switch enforced by basic helix-loop-helix and ACT-domain mediated dimerizations of the maize transcription factor R. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2091-7.	7.1	92
53	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.	3.4	87
54	The Identification of Maize and <i>Arabidopsis</i> Type I FLAVONE SYNTHASEs Links Flavones with Hormones and Biotic Interactions. <i>Plant Physiology</i> , 2015, 169, 1090-1107.	4.8	87

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55	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.	7.1	82
56	MYB31/MYB42 Syntelogs Exhibit Divergent Regulation of Phenylpropanoid Genes in Maize, Sorghum and Rice. <i>Scientific Reports</i> , 2016, 6, 28502.	3.3	81
57	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.	4.8	79
58	Grass phenylpropanoids: Regulate before using!. <i>Plant Science</i> , 2012, 184, 112-120.	3.6	79
59	Helix-loop-helix/basic helix-loop-helix transcription factor network represses cell elongation in <i>Arabidopsis</i> through an apparent incoherent feed-forward loop. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2824-2829.	7.1	76
60	A chemical complementation approach reveals genes and interactions of flavonoids with other pathways. <i>Plant Journal</i> , 2013, 74, 383-397.	5.7	74
61	Flavonols Protect <i>Arabidopsis</i> Plants against UV-B Deleterious Effects. <i>Molecular Plant</i> , 2013, 6, 1376-1379.	8.3	74
62	Transcriptional regulation of PIN genes by FOUR LIPS and MYB88 during <i>Arabidopsis</i> root gravitropism. <i>Nature Communications</i> , 2015, 6, 8822.	12.8	74
63	A Maize Gene Regulatory Network for Phenolic Metabolism. <i>Molecular Plant</i> , 2017, 10, 498-515.	8.3	74
64	Isolation and characterization of a maize gene encoding chalcone flavanone isomerase. <i>Molecular Genetics and Genomics</i> , 1994, 242, 1-8.	2.4	70
65	A coherent transcriptional feed-forward motif model for mediating auxin-sensitive PIN3 expression during lateral root development. <i>Nature Communications</i> , 2015, 6, 8821.	12.8	70
66	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.	4.1	69
67	Standardized Method for High-throughput Sterilization of <i>Arabidopsis</i> Seeds. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	69
68	Expression of flavonoid 3 ^o -hydroxylase is controlled by P1, the regulator of 3-deoxyflavonoid biosynthesis in maize. <i>BMC Plant Biology</i> , 2012, 12, 196.	3.6	65
69	Core Promoter Plasticity Between Maize Tissues and Genotypes Contrasts with Predominance of Sharp Transcription Initiation Sites. <i>Plant Cell</i> , 2015, 27, 3309-3320.	6.6	65
70	Metabolic engineering to enhance the value of plants as green factories. <i>Metabolic Engineering</i> , 2015, 27, 83-91.	7.0	65
71	Identification and Characterization of Maize <i>salmon silks</i> Genes Involved in Insecticidal Maysin Biosynthesis. <i>Plant Cell</i> , 2016, 28, 1297-1309.	6.6	64
72	Source verification of misidentified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011, 67, 554-566.	5.7	63

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73	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.	7.3	61
74	Transcriptional repression of the APC/C activator CCS52A1 promotes active termination of cell growth. <i>EMBO Journal</i> , 2012, 31, 4488-4501.	7.8	60
75	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	6.6	60
76	Light-induced morphological alteration in anthocyanin-accumulating vacuoles of maize cells. <i>BMC Plant Biology</i> , 2005, 5, 7.	3.6	58
77	Interplay of MYB factors in differential cell expansion, and consequences for tomato fruit development. <i>Plant Journal</i> , 2011, 68, 337-350.	5.7	55
78	The Maize TFome development of a transcription factor open reading frame collection for functional genomics. <i>Plant Journal</i> , 2014, 80, 356-366.	5.7	55
79	Flavone-rich maize: an opportunity to improve the nutritional value of an important commodity crop. <i>Frontiers in Plant Science</i> , 2014, 5, 440.	3.6	54
80	Apigenin produced by maize flavone synthase I and II protects plants against UVB-induced damage. <i>Plant, Cell and Environment</i> , 2019, 42, 495-508.	5.7	54
81	Handling Arabidopsis Plants: Growth, Preservation of Seeds, Transformation, and Genetic Crosses. <i>Methods in Molecular Biology</i> , 2014, 1062, 3-25.	0.9	54
82	Topological and statistical analyses of gene regulatory networks reveal unifying yet quantitatively different emergent properties. <i>PLoS Computational Biology</i> , 2018, 14, e1006098.	3.2	48
83	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.	4.4	46
84	A Recommendation for Naming Transcription Factor Proteins in the Grasses. <i>Plant Physiology</i> , 2009, 149, 4-6.	4.8	45
85	Combinatorial control of plant gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 31-40.	1.9	44
86	Transposon Insertions in the Promoter of the <i>Zea mays a1</i> Gene Differentially Affect Transcription by the Myb Factors P and C1. <i>Genetics</i> , 2002, 161, 793-801.	2.9	43
87	Emergence of Switch-Like Behavior in a Large Family of Simple Biochemical Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1002039.	3.2	41
88	From plant gene regulatory grids to network dynamics. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 454-465.	1.9	41
89	Rhamnose in plants - from biosynthesis to diverse functions. <i>Plant Science</i> , 2021, 302, 110687.	3.6	41
90	The tomato early fruit specific gene <i>Lefsm1</i> defines a novel class of plant-specific SANT/MYB domain proteins. <i>Planta</i> , 2005, 221, 197-211.	3.2	40

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91	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.	0.9	38
92	Evolution and Expression of Tandem Duplicated Maize Flavonol Synthase Genes. <i>Frontiers in Plant Science</i> , 2012, 3, 101.	3.6	36
93	Sub-cellular trafficking of phytochemicals explored using auto-fluorescent compounds in maize cells. <i>BMC Plant Biology</i> , 2003, 3, 10.	3.6	35
94	Challenges and opportunities for improving food quality and nutrition through plant biotechnology. <i>Current Opinion in Biotechnology</i> , 2017, 44, 124-129.	6.6	34
95	Challenges of Translating Gene Regulatory Information into Agronomic Improvements. <i>Trends in Plant Science</i> , 2019, 24, 1075-1082.	8.8	34
96	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
97	Trafficking and Sequestration of Anthocyanins. <i>Natural Product Communications</i> , 2008, 3, 1934578X0800300.	0.5	33
98	The capacity for multistability in small gene regulatory networks. <i>BMC Systems Biology</i> , 2009, 3, 96.	3.0	33
99	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.	6.6	32
100	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.	3.7	32
101	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.	3.8	30
102	Manipulating the accumulation of phenolics in maize cultured cells using transcription factors. <i>Biochemical Engineering Journal</i> , 2003, 14, 207-216.	3.6	30
103	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2022, 34, 514-534.	6.6	30
104	Chapter three Regulation of anthocyanin pigmentation. <i>Recent Advances in Phytochemistry</i> , 2003, 37, 59-78.	0.5	29
105	The word landscape of the non-coding segments of the <i>Arabidopsis thaliana</i> genome. <i>BMC Genomics</i> , 2009, 10, 463.	2.8	28
106	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.	8.9	26
107	Comparison of ESTs from juvenile and adult phases of the giant unicellular green alga <i>Acetabularia acetabulum</i> . <i>BMC Plant Biology</i> , 2004, 4, 3.	3.6	25
108	Plant specialized metabolism. <i>Plant Science</i> , 2020, 298, 110579.	3.6	25

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109	Gene-Specific and Genome-Wide ChIP Approaches to Study Plant Transcriptional Networks. <i>Methods in Molecular Biology</i> , 2009, 553, 3-12.	0.9	25
110	Ubiquitin expression in <i>Neurospora crassa</i> : cloning and sequencing of a polyubiquitin gene. <i>Nucleic Acids Research</i> , 1989, 17, 6153-6165.	14.5	24
111	Modeling temporal and hormonal regulation of plant transcriptional response to wounding. <i>Plant Cell</i> , 2022, 34, 867-888.	6.6	22
112	Characterization of Anthocyanidin Synthase (ANS) Gene and anthocyanidin in rare medicinal plant- <i>Saussurea medusa</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 89, 63-73.	2.3	20
113	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
114	Identification of biochemical features of defective <i>Coffea arabica</i> L. beans. <i>Food Research International</i> , 2017, 95, 59-67.	6.2	20
115	Using fluorescence lifetime microscopy to study the subcellular localization of anthocyanins. <i>Plant Journal</i> , 2016, 88, 895-903.	5.7	19
116	<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.	3.6	19
117	High-resolution computational imaging of leaf hair patterning using polarized light microscopy. <i>Plant Journal</i> , 2013, 73, 701-708.	5.7	17
118	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.	12.8	17
119	Expression and Molecular Characterization of ZmMYB-IF35 and Related R2R3-MYB Transcription Factors. <i>Molecular Biotechnology</i> , 2007, 37, 155-164.	2.4	16
120	Components and Mechanisms of Regulation of Gene Expression. <i>Methods in Molecular Biology</i> , 2010, 674, 23-32.	0.9	15
121	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
122	Cloning and characterization of a flavanone 3-hydroxylase gene from <i>Saussurea medusa</i> . <i>DNA Sequence</i> , 2005, 16, 121-129.	0.7	14
123	Serial ChIP as a tool to investigate the co-localization or exclusion of proteins on plant genes. <i>Plant Methods</i> , 2008, 4, 25.	4.3	14
124	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.	3.6	14
125	RNase P as a tool for disruption of gene expression in maize cells. <i>Biochemical Journal</i> , 2004, 380, 611-616.	3.7	13
126	Exploring <i>Camelina sativa</i> lipid metabolism regulation by combining gene co-expression and DNA affinity purification analyses. <i>Plant Journal</i> , 2022, 110, 589-606.	5.7	13

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127	The BIF Domain in Plant bHLH Proteins Is an ACT-Like Domain. <i>Plant Cell</i> , 2017, 29, 1800-1802.	6.6	12
128	The cDNA sequence and expression of an ubiquitin-tail gene fusion in <i>Neurospora crassa</i> . <i>Gene</i> , 1991, 102, 133-137.	2.2	11
129	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. <i>Plant Cell</i> , 1998, 10, 721.	6.6	11
130	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	4.8	11
131	Discovery of modules involved in the biosynthesis and regulation of maize phenolic compounds. <i>Plant Science</i> , 2020, 291, 110364.	3.6	11
132	Microautophagy Mediates Vacuolar Delivery of Storage Proteins in Maize Aleurone Cells. <i>Frontiers in Plant Science</i> , 2022, 13, 833612.	3.6	11
133	Arabidopsis 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.	3.6	10
134	Diversity of genetic lesions characterizes new Arabidopsis flavonoid pigment mutant alleles from T-DNA collections. <i>Plant Science</i> , 2020, 291, 110335.	3.6	10
135	Arabidopsis Database and Stock Resources. <i>Methods in Molecular Biology</i> , 2014, 1062, 65-96.	0.9	10
136	Flavonols drive plant microevolution. <i>Nature Genetics</i> , 2016, 48, 112-113.	21.4	9
137	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.	3.4	9
138	Differential gene expression promoted by cycloheximide in <i>Neurospora crassa</i> . <i>Experimental Mycology</i> , 1987, 11, 122-127.	1.6	8
139	Establishing the Architecture of Plant Gene Regulatory Networks. <i>Methods in Enzymology</i> , 2016, 576, 251-304.	1.0	8
140	News from the plant world: Listening to transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1-2.	1.9	8
141	Arabidopsis MATE 45 antagonizes local abscisic acid signaling to mediate development and abiotic stress responses. <i>Plant Direct</i> , 2018, 2, e00087.	1.9	8
142	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, .	3.0	7
143	The challenges faced by living stock collections in the USA. <i>ELife</i> , 2017, 6, .	6.0	7
144	Metabolite Profiling as a Functional Genomics Tool. , 2003, 236, 415-426.		6

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145	Covalent attachment of the plant natural product naringenin to small glass and ceramic beads. <i>BMC Chemical Biology</i> , 2005, 5, 3.	1.6	6
146	Following Phenotypes: An Exploration of Mendelian Genetics Using Arabidopsis Plants. <i>American Biology Teacher</i> , 2018, 80, 291-300.	0.2	6
147	Participation of Phytochemicals in Plant Development and Growth. , 2009, , 269-279.		6
148	Important biological information uncovered in previously unaligned reads from chromatin immunoprecipitation experiments (ChIP-Seq). <i>Scientific Reports</i> , 2015, 5, 8635.	3.3	5
149	Natural variation and improved genome annotation of the emerging biofuel crop field pennycress (<i>Thlaspi arvense</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	5
150	Plant biotechnology – Predictive, green and quantitative. <i>Current Opinion in Biotechnology</i> , 2008, 19, 129-130.	6.6	4
151	Turning over a new leaf in plant genomics. <i>Genome Biology</i> , 2013, 14, 403.	8.8	4
152	The Plant Genome: Decoding the Transcriptional Hardwiring. , 0, , 196-228.		4
153	A novel reverse-genetic approach (SIMF) identifies Mutator insertions in new Myb genes. <i>Planta</i> , 2000, 211, 887-893.	3.2	3
154	Imaging Vacuolar Anthocyanins with Fluorescence Lifetime Microscopy (FLIM). <i>Methods in Molecular Biology</i> , 2018, 1789, 131-141.	0.9	3
155	Maize Transcription Factors. , 2009, , 693-713.		3
156	Protocol for the Generation of a Transcription Factor Open Reading Frame Collection (TFome). <i>Bio-protocol</i> , 2015, 5, .	0.4	3
157	Design of Knowledge Bases for Plant Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2017, 1629, 207-223.	0.9	1
158	Genome-Wide TSS Identification in Maize. <i>Methods in Molecular Biology</i> , 2018, 1830, 239-256.	0.9	1
159	Encyclopedias of DNA Elements for Plant Genomes. <i>Science, Engineering, and Biology Informatics</i> , 2011, , 159-178.	0.1	1
160	Transcription Factors, Gene Regulatory Networks and Agronomic Traits. <i>Advances in Agroecology</i> , 2011, , 65-94.	0.3	1
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