

Erich Grotewold

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

165
papers

15,669
citations

56
h-index

124
g-index

200
ext. papers

18,635
ext. citations

8
avg. IF

7.01
L-index

#	Paper	IF	Citations
165	MYB transcription factors in Arabidopsis. <i>Trends in Plant Science</i> , 2010 , 15, 573-81	13.1	1731
164	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010 , 463, 763-850.4	50.4	1399
163	Root exudation and rhizosphere biology. <i>Plant Physiology</i> , 2003 , 132, 44-51	6.6	994
162	The genetics and biochemistry of floral pigments. <i>Annual Review of Plant Biology</i> , 2006 , 57, 761-80	30.7	930
161	Evolutionary and comparative analysis of MYB and bHLH plant transcription factors. <i>Plant Journal</i> , 2011 , 66, 94-116	6.9	685
160	How genes paint flowers and seeds. <i>Trends in Plant Science</i> , 1998 , 3, 212-217	13.1	653
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, 543-53	56.2	565
158	Flavonoids as developmental regulators. <i>Current Opinion in Plant Biology</i> , 2005 , 8, 317-23	9.9	439
157	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. <i>Plant Cell</i> , 1998 , 10, 721-740	11.6	301
156	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. <i>BMC Bioinformatics</i> , 2003 , 4, 25	3.6	298
155	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, 13579-84	11.5	259
154	The TTG1-bHLH-MYB complex controls trichome cell fate and patterning through direct targeting of regulatory loci. <i>Development (Cambridge)</i> , 2008 , 135, 1991-9	6.6	250
153	Apigenin blocks lipopolysaccharide-induced lethality in vivo and proinflammatory cytokines expression by inactivating NF-kappaB through the suppression of p65 phosphorylation. <i>Journal of Immunology</i> , 2007 , 179, 7121-7	5.3	247
152	AGRIS: the Arabidopsis Gene Regulatory Information Server, an update. <i>Nucleic Acids Research</i> , 2011 , 39, D1118-22	20.1	234
151	AGRIS and AtRegNet. a platform to link cis-regulatory elements and transcription factors into regulatory networks. <i>Plant Physiology</i> , 2006 , 140, 818-29	6.6	210
150	GRASSIUS: a platform for comparative regulatory genomics across the grasses. <i>Plant Physiology</i> , 2009 , 149, 171-80	6.6	198
149	<i>Brachypodium</i> as a model for the grasses: today and the future. <i>Plant Physiology</i> , 2011 , 157, 3-13	6.6	190

148	Unraveling the KNOTTED1 regulatory network in maize meristems. <i>Genes and Development</i> , 2012 , 26, 1685-90	12.6	179
147	ZmMYB31 directly represses maize lignin genes and redirects the phenylpropanoid metabolic flux. <i>Plant Journal</i> , 2010 , 64, 633-44	6.9	178
146	A systems approach reveals regulatory circuitry for Arabidopsis trichome initiation by the GL3 and GL1 selectors. <i>PLoS Genetics</i> , 2009 , 5, e1000396	6	168
145	Participation of the Arabidopsis bHLH factor GL3 in trichome initiation regulatory events. <i>Plant Physiology</i> , 2007 , 145, 736-46	6.6	151
144	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, 1323-35	6.6	151
143	Genome wide analysis of Arabidopsis core promoters. <i>BMC Genomics</i> , 2005 , 6, 25	4.5	150
142	Maize R2R3 Myb genes: Sequence analysis reveals amplification in the higher plants. <i>Genetics</i> , 1999 , 153, 427-44	4	132
141	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016 , 209, 921-44	9.8	128
140	Apigenin-induced-apoptosis is mediated by the activation of PKCdelta and caspases in leukemia cells. <i>Biochemical Pharmacology</i> , 2006 , 72, 681-92	6	127
139	Recently duplicated maize R2R3 Myb genes provide evidence for distinct mechanisms of evolutionary divergence after duplication. <i>Plant Physiology</i> , 2003 , 131, 610-20	6.6	127
138	Transcription factors for predictive plant metabolic engineering: are we there yet?. <i>Current Opinion in Biotechnology</i> , 2008 , 19, 138-44	11.4	123
137	Flavones: From Biosynthesis to Health Benefits. <i>Plants</i> , 2016 , 5,	4.5	121
136	A genome-wide regulatory framework identifies maize pericarp color1 controlled genes. <i>Plant Cell</i> , 2012 , 24, 2745-64	11.6	120
135	Inhibition of AtMYB2 DNA-binding by nitric oxide involves cysteine S-nitrosylation. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 361, 1048-53	3.4	115
134	Plant metabolic diversity: a regulatory perspective. <i>Trends in Plant Science</i> , 2005 , 10, 57-62	13.1	115
133	Regulation of cell proliferation in the stomatal lineage by the Arabidopsis MYB FOUR LIPS via direct targeting of core cell cycle genes. <i>Plant Cell</i> , 2010 , 22, 2306-21	11.6	112
132	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	14.4	108
131	Anthocyanin Vacuolar Inclusions Form by a Microautophagy Mechanism. <i>Plant Cell</i> , 2015 , 27, 2545-59	11.6	103

130	Regulatory modules controlling maize inflorescence architecture. <i>Genome Research</i> , 2014 , 24, 431-43	9.7	102
129	Different mechanisms participate in the R-dependent activity of the R2R3 MYB transcription factor C1. <i>Journal of Biological Chemistry</i> , 2004 , 279, 48205-13	5.4	101
128	Cloning and characterization of a UV-B-inducible maize flavonol synthase. <i>Plant Journal</i> , 2010 , 62, 77-91	6.9	96
127	Not all anthocyanins are born equal: distinct patterns induced by stress in Arabidopsis. <i>Planta</i> , 2014 , 240, 931-40	4.7	95
126	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, 28964-74	5.4	90
125	Identification of a bifunctional maize C- and O-glucosyltransferase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31678-88	5.4	88
124	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	11.5	87
123	Developmental regulation of CYCA2s contributes to tissue-specific proliferation in Arabidopsis. <i>EMBO Journal</i> , 2011 , 30, 3430-41	13	86
122	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	4.7	84
121	Two cysteines in plant R2R3 MYB domains participate in REDOX-dependent DNA binding. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37878-85	5.4	81
120	WIND1 Promotes Shoot Regeneration through Transcriptional Activation of in Arabidopsis. <i>Plant Cell</i> , 2017 , 29, 54-69	11.6	80
119	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	6.6	79
118	Abiotic stresses induce different localizations of anthocyanins in Arabidopsis. <i>Plant Signaling and Behavior</i> , 2015 , 10, e1027850	2.5	75
117	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, 563-71	5.4	73
116	Newly discovered plant c-myb-like genes rewrite the evolution of the plant myb gene family. <i>Plant Physiology</i> , 1999 , 121, 21-4	6.6	72
115	Role of the stomatal development regulators FLP/MYB88 in abiotic stress responses. <i>Plant Journal</i> , 2010 , 64, 731-9	6.9	71
114	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, 17222-7	11.5	70
113	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	11.5	64

112	A chemical complementation approach reveals genes and interactions of flavonoids with other pathways. <i>Plant Journal</i> , 2013 , 74, 383-97	6.9	61
111	Isolation and characterization of a maize gene encoding chalcone flavonone isomerase. <i>Molecular Genetics and Genomics</i> , 1994 , 242, 1-8		58
110	Metabolic engineering to enhance the value of plants as green factories. <i>Metabolic Engineering</i> , 2015 , 27, 83-91	9.7	56
109	A MYB/ZML Complex Regulates Wound-Induced Lignin Genes in Maize. <i>Plant Cell</i> , 2015 , 27, 3245-59	11.6	55
108	Source verification of mis-identified Arabidopsis thaliana accessions. <i>Plant Journal</i> , 2011 , 67, 554-66	6.9	53
107	The Identification of Maize and Arabidopsis Type I FLAVONE SYNTHASEs Links Flavones with Hormones and Biotic Interactions. <i>Plant Physiology</i> , 2015 , 169, 1090-107	6.6	49
106	The Maize TFome--development of a transcription factor open reading frame collection for functional genomics. <i>Plant Journal</i> , 2014 , 80, 356-66	6.9	49
105	Grass phenylpropanoids: regulate before using!. <i>Plant Science</i> , 2012 , 184, 112-20	5.3	48
104	Expression of flavonoid 3Rhydroxylase is controlled by P1, the regulator of 3-deoxyflavonoid biosynthesis in maize. <i>BMC Plant Biology</i> , 2012 , 12, 196	5.3	48
103	Light-induced morphological alteration in anthocyanin-accumulating vacuoles of maize cells. <i>BMC Plant Biology</i> , 2005 , 5, 7	5.3	46
102	Transcriptional regulation of PIN genes by FOUR LIPS and MYB88 during Arabidopsis root gravitropism. <i>Nature Communications</i> , 2015 , 6, 8822	17.4	45
101	A coherent transcriptional feed-forward motif model for mediating auxin-sensitive PIN3 expression during lateral root development. <i>Nature Communications</i> , 2015 , 6, 8821	17.4	45
100	Flavonols protect Arabidopsis plants against UV-B deleterious effects. <i>Molecular Plant</i> , 2013 , 6, 1376-9	14.4	44
99	Transcriptional repression of the APC/C activator CCS52A1 promotes active termination of cell growth. <i>EMBO Journal</i> , 2012 , 31, 4488-501	13	44
98	Flavone-rich maize: an opportunity to improve the nutritional value of an important commodity crop. <i>Frontiers in Plant Science</i> , 2014 , 5, 440	6.2	43
97	Dietary Apigenin Exerts Immune-Regulatory Activity in Vivo by Reducing NF-B Activity, Halting Leukocyte Infiltration and Restoring Normal Metabolic Function. <i>International Journal of Molecular Sciences</i> , 2016 , 17, 323	6.3	43
96	Identification and Characterization of Maize salmon silks Genes Involved in Insecticidal Maysin Biosynthesis. <i>Plant Cell</i> , 2016 , 28, 1297-309	11.6	40
95	Helix-loop-helix/basic helix-loop-helix transcription factor network represses cell elongation in Arabidopsis through an apparent incoherent feed-forward loop. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2824-9	11.5	38

94	Apigenin induces DNA damage through the PKC-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, 1571-80	6	38
93	Core Promoter Plasticity Between Maize Tissues and Genotypes Contrasts with Predominance of Sharp Transcription Initiation Sites. <i>Plant Cell</i> , 2015 , 27, 3309-20	11.6	37
92	Emergence of switch-like behavior in a large family of simple biochemical networks. <i>PLoS Computational Biology</i> , 2011 , 7, e1002039	5	37
91	Transposon insertions in the promoter of the Zea mays a1 gene differentially affect transcription by the Myb factors P and C1. <i>Genetics</i> , 2002 , 161, 793-801	4	37
90	The tomato early fruit specific gene Lefsm1 defines a novel class of plant-specific SANT/MYB domain proteins. <i>Planta</i> , 2005 , 221, 197-211	4.7	36
89	A recommendation for naming transcription factor proteins in the grasses. <i>Plant Physiology</i> , 2009 , 149, 4-6	6.6	35
88	MYB31/MYB42 Syntelogs Exhibit Divergent Regulation of Phenylpropanoid Genes in Maize, Sorghum and Rice. <i>Scientific Reports</i> , 2016 , 6, 28502	4.9	34
87	A Maize Gene Regulatory Network for Phenolic Metabolism. <i>Molecular Plant</i> , 2017 , 10, 498-515	14.4	34
86	Interplay of MYB factors in differential cell expansion, and consequences for tomato fruit development. <i>Plant Journal</i> , 2011 , 68, 337-50	6.9	34
85	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	9.8	34
84	From plant gene regulatory grids to network dynamics. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012 , 1819, 454-65	6	32
83	Handling Arabidopsis plants: growth, preservation of seeds, transformation, and genetic crosses. <i>Methods in Molecular Biology</i> , 2014 , 1062, 3-25	1.4	32
82	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	8.4	32
81	Standardized Method for High-throughput Sterilization of Arabidopsis Seeds. <i>Journal of Visualized Experiments</i> , 2017 ,	1.6	31
80	Sub-cellular trafficking of phytochemicals explored using auto-fluorescent compounds in maize cells. <i>BMC Plant Biology</i> , 2003 , 3, 10	5.3	30
79	Topological and statistical analyses of gene regulatory networks reveal unifying yet quantitatively different emergent properties. <i>PLoS Computational Biology</i> , 2018 , 14, e1006098	5	29
78	Challenges and opportunities for improving food quality and nutrition through plant biotechnology. <i>Current Opinion in Biotechnology</i> , 2017 , 44, 124-129	11.4	28
77	Evolution and expression of tandem duplicated maize flavonol synthase genes. <i>Frontiers in Plant Science</i> , 2012 , 3, 101	6.2	28

76	Manipulating the accumulation of phenolics in maize cultured cells using transcription factors. <i>Biochemical Engineering Journal</i> , 2003 , 14, 207-216	4.2	28
75	Combinatorial control of plant gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 31-40	6	27
74	Essential dynamics from NMR clusters: dynamic properties of the Myb DNA-binding domain and a hinge-bending enhancing variant. <i>Methods</i> , 1998 , 14, 318-28	4.6	26
73	The capacity for multistability in small gene regulatory networks. <i>BMC Systems Biology</i> , 2009 , 3, 96	3.5	25
72	Fungal Zuotin proteins evolved from MIDA1-like factors by lineage-specific loss of MYB domains. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1401-12	8.3	25
71	A possible hot spot for Ac insertion in the maize P gene. <i>Molecular Genetics and Genomics</i> , 1991 , 230, 329-31		25
70	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, 249-58	1.4	24
69	Chapter three Regulation of anthocyanin pigmentation. <i>Recent Advances in Phytochemistry</i> , 2003 , 37, 59-78		22
68	Gene-specific and genome-wide ChIP approaches to study plant transcriptional networks. <i>Methods in Molecular Biology</i> , 2009 , 553, 3-12	1.4	22
67	Ubiquitin expression in <i>Neurospora crassa</i> : cloning and sequencing of a polyubiquitin gene. <i>Nucleic Acids Research</i> , 1989 , 17, 6153-65	20.1	21
66	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020 , 32, 1377-1396	11.6	20
65	The word landscape of the non-coding segments of the <i>Arabidopsis thaliana</i> genome. <i>BMC Genomics</i> , 2009 , 10, 463	4.5	20
64	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	5.3	18
63	POPcorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <i>International Journal of Plant Genomics</i> , 2011 , 2011, 923035		17
62	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	4.5	17
61	Challenges of Translating Gene Regulatory Information into Agronomic Improvements. <i>Trends in Plant Science</i> , 2019 , 24, 1075-1082	13.1	16
60	Trafficking and Sequestration of Anthocyanins. <i>Natural Product Communications</i> , 2008 , 3, 1934578X0800390		16
59	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	2.7	16

58	Identification of biochemical features of defective <i>Coffea arabica</i> L. beans. <i>Food Research International</i> , 2017 , 95, 59-67	7	14
57	Expression and molecular characterization of ZmMYB-IF35 and related R2R3-MYB transcription factors. <i>Molecular Biotechnology</i> , 2007 , 37, 155-64	3	14
56	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	11.6	13
55	RNase P as a tool for disruption of gene expression in maize cells. <i>Biochemical Journal</i> , 2004 , 380, 611-6	3.8	13
54	Chapter Five Transcription factors and metabolic engineering: Novel applications for ancient tools. <i>Recent Advances in Phytochemistry</i> , 2001 , 35, 79-109		13
53	Using fluorescence lifetime microscopy to study the subcellular localization of anthocyanins. <i>Plant Journal</i> , 2016 , 88, 895-903	6.9	13
52	Arabidopsis 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	6.2	12
51	Cloning and characterization of a flavanone 3-hydroxylase gene from <i>Saussurea medusa</i> . <i>DNA Sequence</i> , 2005 , 16, 121-9		12
50	High-resolution computational imaging of leaf hair patterning using polarized light microscopy. <i>Plant Journal</i> , 2013 , 73, 701-8	6.9	11
49	Components and mechanisms of regulation of gene expression. <i>Methods in Molecular Biology</i> , 2010 , 674, 23-32	1.4	11
48	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017 , 175, 1499-1509	6.6	10
47	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	5.3	10
46	Anthocyanin Biosynthesis, Regulation, and Transport: New Insights from Model Species 2012 , 143-160		10
45	Serial ChIP as a tool to investigate the co-localization or exclusion of proteins on plant genes. <i>Plant Methods</i> , 2008 , 4, 25	5.8	10
44	Engineering Secondary Metabolism in Maize Cells by Ectopic Expression of Transcription Factors. <i>Plant Cell</i> , 1998 , 10, 721	11.6	10
43	The cDNA sequence and expression of an ubiquitin-tail gene fusion in <i>Neurospora crassa</i> . <i>Gene</i> , 1991 , 102, 133-7	3.8	10
42	Rhamnose in plants - from biosynthesis to diverse functions. <i>Plant Science</i> , 2021 , 302, 110687	5.3	10
41	Arabidopsis database and stock resources. <i>Methods in Molecular Biology</i> , 2014 , 1062, 65-96	1.4	9

40	Synergy between the anthocyanin and RDR6/SGS3/DCL4 siRNA pathways expose hidden features of Arabidopsis carbon metabolism. <i>Nature Communications</i> , 2020 , 11, 2456	17.4	6
39	Differential gene expression promoted by cycloheximide in <i>Neurospora crassa</i> . <i>Experimental Mycology</i> , 1987 , 11, 122-127		6
38	Cis-regulatory sequences in plants: their importance, discovery, and future challenges.. <i>Plant Cell</i> , 2021 ,	11.6	6
37	The challenges faced by living stock collections in the USA. <i>ELife</i> , 2017 , 6,	8.9	6
36	Diversity of genetic lesions characterizes new Arabidopsis flavonoid pigment mutant alleles from T-DNA collections. <i>Plant Science</i> , 2020 , 291, 110335	5.3	6
35	Participation of Phytochemicals in Plant Development and Growth 2009 , 269-279		6
34	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	5.3	5
33	Flavonoid Dietetics: Mechanisms and Emerging Roles of Plant Nutraceuticals 2015 , 93-126		5
32	Important biological information uncovered in previously unaligned reads from chromatin immunoprecipitation experiments (ChIP-Seq). <i>Scientific Reports</i> , 2015 , 5, 8635	4.9	5
31	Flavonols drive plant microevolution. <i>Nature Genetics</i> , 2016 , 48, 112-3	36.3	5
30	Metabolite profiling as a functional genomics tool. <i>Methods in Molecular Biology</i> , 2003 , 236, 415-26	1.4	5
29	Covalent attachment of the plant natural product naringenin to small glass and ceramic beads. <i>BMC Chemical Biology</i> , 2005 , 5, 3		5
28	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2021 ,	11.6	5
27	Establishing the Architecture of Plant Gene Regulatory Networks. <i>Methods in Enzymology</i> , 2016 , 576, 251-304	1.7	5
26	The BIF Domain in Plant bHLH Proteins Is an ACT-Like Domain. <i>Plant Cell</i> , 2017 , 29, 1800-1802	11.6	4
25	Discovery of modules involved in the biosynthesis and regulation of maize phenolic compounds. <i>Plant Science</i> , 2020 , 291, 110364	5.3	4
24	Arabidopsis MATE45 antagonizes local abscisic acid signaling to mediate development and abiotic stress responses. <i>Plant Direct</i> , 2018 , 2, e00087	3.3	4
23	A novel reverse-genetic approach (SIMF) identifies Mutator insertions in new Myb genes. <i>Planta</i> , 2000 , 211, 887-93	4.7	3

22	Modeling temporal and hormonal regulation of plant transcriptional response to wounding. <i>Plant Cell</i> , 2021 ,	11.6	3
21	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	5.4	3
20	Imaging Vacuolar Anthocyanins with Fluorescence Lifetime Microscopy (FLIM). <i>Methods in Molecular Biology</i> , 2018 , 1789, 131-141	1.4	3
19	Plant Functional Genomics 2003 ,		2
18	Protocol for the Generation of a Transcription Factor Open Reading Frame Collection (TFome). <i>Bio-protocol</i> , 2015 , 5,	0.9	2
17	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,	5	2
16	Following Phenotypes: An Exploration of Mendelian Genetics Using Arabidopsis Plants. <i>American Biology Teacher</i> , 2018 , 80, 291-300	0.3	2
15	The Plant Genome: Decoding the Transcriptional Hardwiring 196-228		2
14	Maize Transcription Factors 2009 , 693-713		2
13	Exploring <i>Camelina sativa</i> lipid metabolism regulation by combining gene co-expression and DNA affinity purification analyses.. <i>Plant Journal</i> , 2022 ,	6.9	1
12	Encyclopedias of DNA Elements for Plant Genomes. <i>Science, Engineering, and Biology Informatics</i> , 2011 , 159-178		1
11	Transcription Factors, Gene Regulatory Networks and Agronomic Traits. <i>Advances in Agroecology</i> , 2011 , 65-94		1
10	Co-expression signatures of combinatorial gene regulation		1
9	Microautophagy Mediates Vacuolar Delivery of Storage Proteins in Maize Aleurone Cells.. <i>Frontiers in Plant Science</i> , 2022 , 13, 833612	6.2	0
8	Design of Knowledge Bases for Plant Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2017 , 1629, 207-223	1.4	
7	Small RNAs 2015 , 161-172		
6	Control of Transcription Factor Activity 2015 , 149-160		
5	Making mRNAs [Control of Transcription by RNA Polymerase II 2015 , 121-131		

- 4 Genome-Wide TSS Identification in Maize. *Methods in Molecular Biology*, **2018**, 1830, 239-256 1.4
- 3 Identification of Human-Flavonoid Targets Using an Innovative Approach Reveals New Mechanisms Involved in Their Anti-Inflammatory Activities. *FASEB Journal*, **2012**, 26, 251.5 0.9
- 2 The Plant Genome: Decoding the Transcriptional Hardwiring **2018**, 196-228
- 1 Normalizing and Correcting Variable and Complex LCMS Metabolomic Data with the R Package pseudoDrift. *Metabolites*, **2022**, 12, 435 5.6