

Bernd Weisshaar

List of Publications by Year in descending order

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161
papers

27,205
citations

13865

67
h-index

6300

158
g-index

201
all docs

201
docs citations

201
times ranked

20183
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. BMC Genomics, 2022, 23, 113.	2.8	10
2	Mapping-by-Sequencing Reveals Genomic Regions Associated with Seed Quality Parameters in Brassica napus. Genes, 2022, 13, 1131.	2.4	4
3	The transition to flowering in winter rapeseed during vernalization. Plant, Cell and Environment, 2021, 44, 506-518.	5.7	19
4	Reference-based QUantification Of gene Dispensability (QUOD). Plant Methods, 2021, 17, 18.	4.3	3
5	Transcriptomic analysis of temporal shifts in berry development between two grapevine cultivars of the Pinot family reveals potential genes controlling ripening time. BMC Plant Biology, 2021, 21, 327.	3.6	8
6	Large scale genomic rearrangements in selected Arabidopsis thaliana T-DNA lines are caused by T-DNA insertion mutagenesis. BMC Genomics, 2021, 22, 599.	2.8	42
7	Functional Characterisation of Banana (Musa spp.) 2-Oxoglutarate-Dependent Dioxygenases Involved in Flavonoid Biosynthesis. Frontiers in Plant Science, 2021, 12, 701780.	3.6	20
8	A novel, robust and mating-competent Chlamydomonas reinhardtii strain with an enhanced transgene expression capacity for algal biotechnology. Biotechnology Reports (Amsterdam, Netherlands), 2021, 31, e00644.	4.4	10
9	Characterization of the Brassica napus Flavonol Synthase Gene Family Reveals Bifunctional Flavonol Synthases. Frontiers in Plant Science, 2021, 12, 733762.	3.6	24
10	Functional and evolutionary analysis of the Arabidopsis 4R-MYB protein SNAPc4 as part of the SNAP complex. Plant Physiology, 2021, 185, 1002-1020.	4.8	9
11	The R2R3-MYB gene family in banana (Musa acuminata): Genome-wide identification, classification and expression patterns. PLoS ONE, 2020, 15, e0239275.	2.5	39
12	RNA-Seq Time Series of Vitis vinifera Bud Development Reveals Correlation of Expression Patterns with the Local Temperature Profile. Plants, 2020, 9, 1548.	3.5	7
13	Genome Sequencing of Musa acuminata Dwarf Cavendish Reveals a Duplication of a Large Segment of Chromosome 2. G3: Genes, Genomes, Genetics, 2020, 10, 37-42.	1.8	10
14	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar Bârnerâ™. Microbiology Resource Announcements, 2020, 9, .	0.6	3
15	High Contiguity de novo Genome Sequence Assembly of Trifoliate Yam (Dioscorea dumetorum) Using Long Read Sequencing. Genes, 2020, 11, 274.	2.4	54
16	A Partially Phase-Separated Genome Sequence Assembly of the Vitis Rootstock Bârnerâ™ (Vitis riparia Ã— Vitis rotundifolia) Tj ETQq0 0 0 rgBT /Over Science, 2020, 11, 156.	3.6	6
17	Characterization of genes and alleles involved in the control of flowering time in grapevine. PLoS ONE, 2019, 14, e0214703.	2.5	9
18	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the Arabidopsis Thaliana Genome. Genes, 2019, 10, 671.	2.4	15

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19	A chromosome-level sequence assembly reveals the structure of the <i>Arabidopsis thaliana</i> Nd-1 genome and its gene set. <i>PLoS ONE</i> , 2019, 14, e0216233.	2.5	40
20	Crop wild relative populations of <i>Beta vulgaris</i> allow direct mapping of agronomically important genes. <i>Nature Communications</i> , 2017, 8, 15708.	12.8	58
21	The <i>AtMYB12</i> activation domain maps to a short C-terminal region of the transcription factor. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2017, 72, 251-257.	1.4	20
22	Consideration of non-canonical splice sites improves gene prediction on the <i>Arabidopsis thaliana</i> Niederzenz-1 genome sequence. <i>BMC Research Notes</i> , 2017, 10, 667.	1.4	24
23	Evolution of tonoplast $\text{P}^{\text{H}}\text{ATPase}$ transporters involved in vacuolar acidification. <i>New Phytologist</i> , 2016, 211, 1092-1107.	7.3	37
24	Repeat Composition of CenH3-chromatin and H3K9me2-marked heterochromatin in Sugar Beet (<i>Beta</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	32
25	Enhancing the GABI-Kat <i>Arabidopsis thaliana</i> T-DNA Insertion Mutant Database by Incorporating Araport11 Annotation. <i>Plant and Cell Physiology</i> , 2016, 58, pcw205.	3.1	6
26	ReadXplorer 2â€”detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016, 32, 3702-3708.	4.1	96
27	Chloroplast Genome Sequence of <i>Arabidopsis thaliana</i> Accession Landsberg erecta , Assembled from Single-Molecule, Real-Time Sequencing Data. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
28	Analyzing Synthetic Promoters Using <i>Arabidopsis</i> Protoplasts. <i>Methods in Molecular Biology</i> , 2016, 1482, 67-81.	0.9	7
29	Rapid gene identification in sugar beet using deep sequencing of DNA from phenotypic pools selected from breeding panels. <i>BMC Genomics</i> , 2016, 17, 236.	2.8	26
30	Diversification, evolution and methylation of short interspersed nuclear element families in sugar beet and related <i>Amaranthaceae</i> species. <i>Plant Journal</i> , 2016, 85, 229-244.	5.7	29
31	Natural variation in flavonol accumulation in <i>Arabidopsis</i> is determined by the flavonol glucosyltransferase <i>BGLU6</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1505-1517.	4.8	67
32	A De Novo Genome Sequence Assembly of the <i>Arabidopsis thaliana</i> Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. <i>PLoS ONE</i> , 2016, 11, e0164321.	2.5	63
33	SMRT sequencing only de novo assembly of the sugar beet (<i>Beta vulgaris</i>) chloroplast genome. <i>BMC Bioinformatics</i> , 2015, 16, 295.	2.6	34
34	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184.	8.8	148
35	Fast forward genetics to identify mutations causing a high light tolerant phenotype in <i>Chlamydomonas reinhardtii</i> by whole-genome-sequencing. <i>BMC Genomics</i> , 2015, 16, 57.	2.8	56
36	TRANSPARENT TESTA 13 is a tonoplast $\text{P}^{\text{H}}\text{ATPase}$ required for vacuolar deposition of proanthocyanidins in <i>Arabidopsis thaliana</i> seeds. <i>Plant Journal</i> , 2015, 82, 840-849.	5.7	71

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37	The Structural Features of Thousands of T-DNA Insertion Sites Are Consistent with a Double-Strand Break Repair-Based Insertion Mechanism. <i>Molecular Plant</i> , 2015, 8, 1651-1664.	8.3	80
38	An easy-to-use primer design tool to address paralogous loci and T-DNA insertion sites in the genome of <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2014, 10, 28.	4.3	8
39	Genome-wide identification and characterisation of R2R3-MYB genes in sugar beet (<i>Beta vulgaris</i>). <i>BMC Plant Biology</i> , 2014, 14, 249.	3.6	95
40	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	6.6	164
41	The <sc>CHH</sc> motif in sugar beet satellite <sc>DNA</sc>: a modulator for cytosine methylation. <i>Plant Journal</i> , 2014, 78, 937-950.	5.7	17
42	Profiling of extensively diversified plant <sc>LINE</sc>s reveals distinct plant-specific subclades. <i>Plant Journal</i> , 2014, 79, 385-397.	5.7	35
43	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	27.8	569
44	The Genomics Revolution and its Impact on Future Biotechnology. <i>Journal of Biotechnology</i> , 2014, 190, 1.	3.8	1
45	QTL analysis of flowering time and ripening traits suggests an impact of a genomic region on linkage group 1 in <i>Vitis</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 1857-1872.	3.6	44
46	Update on transparent testa mutants from <i>Arabidopsis thaliana</i> : characterisation of new alleles from an isogenic collection. <i>Planta</i> , 2014, 240, 955-970.	3.2	106
47	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. <i>BMC Genomics</i> , 2014, 15, 317.	2.8	19
48	Reliable In Silico Identification of Sequence Polymorphisms and Their Application for Extending the Genetic Map of Sugar Beet (<i>Beta vulgaris</i>). <i>PLoS ONE</i> , 2014, 9, e110113.	2.5	18
49	Highly diverse chromoviruses of <i>Beta vulgaris</i> are classified by chromodomains and chromosomal integration. <i>Mobile DNA</i> , 2013, 4, 8.	3.6	36
50	<sc>GABI</sc>-<sc>DUPLO</sc>: a collection of double mutants to overcome genetic redundancy in <i><sc>A</sc>rabidopsis thaliana</i>. <i>Plant Journal</i> , 2013, 75, 157-171.	5.7	48
51	Toward the identification and regulation of the <i>Arabidopsis thaliana</i> ABI3 regulon. <i>Nucleic Acids Research</i> , 2012, 40, 8240-8254.	14.5	145
52	GABI-Kat SimpleSearch: new features of the <i>Arabidopsis thaliana</i> T-DNA mutant database. <i>Nucleic Acids Research</i> , 2012, 40, D1211-D1215.	14.5	336
53	Evolutionary reshuffling in the Errantivirus lineage Elbe within the <i>Beta vulgaris</i> genome. <i>Plant Journal</i> , 2012, 72, 636-651.	5.7	26
54	Candidate genes within a 143 kb region of the flower sex locus in <i>Vitis</i> . <i>Molecular Genetics and Genomics</i> , 2012, 287, 247-259.	2.1	98

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55	The Role of a Pseudo-Response Regulator Gene in Life Cycle Adaptation and Domestication of Beet. <i>Current Biology</i> , 2012, 22, 1095-1101.	3.9	135
56	Palaeohexaploid ancestry for Caryophyllales inferred from extensive genome-based physical and genetic mapping of the sugar beet genome (<i>Beta vulgaris</i>). <i>Plant Journal</i> , 2012, 70, 528-540.	5.7	58
57	Elongation-related functions of LEAFY COTYLEDON1 during the development of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2012, 71, 427-442.	5.7	133
58	Survey of sugar beet (<i>Beta vulgaris</i> L.) hAT transposons and MITE-like hATpin derivatives. <i>Plant Molecular Biology</i> , 2012, 78, 393-405.	3.9	16
59	COMBINING GENOMICS AND METABOLOMICS FOR THE DISCOVERY OF REGULATORY GENES AND THEIR USE IN METABOLIC ENGINEERING TO PRODUCE 'HEALTHY FOODS'. <i>Acta Horticulturae</i> , 2012, , 73-84.	0.2	3
60	Resources for Reverse Genetics Approaches in <i>Arabidopsis thaliana</i> . , 2011, , 527-560.		1
61	Leucoanthocyanidin Dioxygenase in <i>Arabidopsis thaliana</i> : Characterization of mutant alleles and regulation by MYB-BHLH-TTG1 transcription factor complexes. <i>Gene</i> , 2011, 484, 61-68.	2.2	95
62	Two differentially expressed <i>MATE</i> factor genes from apple complement the <i>Arabidopsis</i> transparent testa12 mutant. <i>Plant Biology</i> , 2011, 13, 42-50.	3.8	38
63	TRANSPARENT TESTA1 interacts with R2R3-MYB factors and affects early and late steps of flavonoid biosynthesis in the endothelium of <i>Arabidopsis thaliana</i> seeds. <i>Plant Journal</i> , 2011, 67, 406-419.	5.7	81
64	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
65	Epigenetic profiling of heterochromatic satellite DNA. <i>Chromosoma</i> , 2011, 120, 409-422.	2.2	31
66	A unique transcriptome: 1782 positions of RNA editing alter 1406 codon identities in mitochondrial mRNAs of the lycophyte <i>Isoetes engelmannii</i> . <i>Nucleic Acids Research</i> , 2011, 39, 2890-2902.	14.5	102
67	Targeted Identification of Short Interspersed Nuclear Element Families Shows Their Widespread Existence and Extreme Heterogeneity in Plant Genomes. <i>Plant Cell</i> , 2011, 23, 3117-3128.	6.6	116
68	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. <i>Theoretical and Applied Genetics</i> , 2010, 121, 549-565.	3.6	6
69	A WD40-repeat gene from <i>Malus domestica</i> is a functional homologue of <i>Arabidopsis thaliana</i> TRANSPARENT TESTA GLABRA1. <i>Plant Cell Reports</i> , 2010, 29, 285-294.	5.6	78
70	Analysis of a cOt-1 library enables the targeted identification of minisatellite and satellite families in <i>Beta vulgaris</i> . <i>BMC Plant Biology</i> , 2010, 10, 8.	3.6	28
71	Expression analysis of flavonoid biosynthesis genes during <i>Arabidopsis thaliana</i> silique and seed development with a primary focus on the proanthocyanidin biosynthetic pathway. <i>BMC Research Notes</i> , 2010, 3, 255.	1.4	48
72	Weird fingers: Functional analysis of WIP domain proteins. <i>FEBS Letters</i> , 2010, 584, 3116-3122.	2.8	35

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73	Analysis of PRODUCTION OF FLAVONOL GLYCOSIDESâ€dependent flavonol glycoside accumulation in <i>Arabidopsis thaliana</i> plants reveals MYB11â€, MYB12â€and MYB111â€independent flavonol glycoside accumulation. <i>New Phytologist</i> , 2010, 188, 985-1000.	7.3	285
74	The <i>Arabidopsis</i> bZIP transcription factor HY5 regulates expression of the PFG1/ MYB12 gene in response to light and ultraviolet-B radiation. <i>Plant, Cell and Environment</i> , 2010, 33, 88-103.	5.7	324
75	The <i>Arabidopsis</i> Thylakoid Protein PAM68 Is Required for Efficient D1 Biogenesis and Photosystem II Assembly. <i>Plant Cell</i> , 2010, 22, 3439-3460.	6.6	116
76	Complete Genome Sequence of <i>Listeria seeligeri</i> , a Nonpathogenic Member of the Genus <i>Listeria</i> . <i>Journal of Bacteriology</i> , 2010, 192, 1473-1474.	2.2	23
77	MYB transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2010, 15, 573-581.	8.8	2,987
78	A trans -splicing group I intron and tRNA-hyperediting in the mitochondrial genome of the lycophyte <i>Isoetes engelmannii</i> . <i>Nucleic Acids Research</i> , 2009, 37, 5093-5104.	14.5	139
79	The Grapevine R2R3-MYB Transcription Factor VvMYBF1 Regulates Flavonol Synthesis in Developing Grape Berries. <i>Plant Physiology</i> , 2009, 151, 1513-1530.	4.8	383
80	<i>Arabidopsis thaliana</i> expresses a second functional flavonol synthase. <i>FEBS Letters</i> , 2009, 583, 1981-1986.	2.8	75
81	Metabolomic and genetic analyses of flavonol synthesis in <i>Arabidopsis thaliana</i> support the in vivo involvement of leucoanthocyanidin dioxygenase. <i>Planta</i> , 2009, 229, 427-445.	3.2	116
82	An abundant and heavily truncated non-LTR retrotransposon (LINE) family in <i>Beta vulgaris</i> . <i>Plant Molecular Biology</i> , 2009, 71, 585-597.	3.9	18
83	Trace2PS and FSA2PS: two software toolkits for converting trace and fsa files to PostScript format. <i>Source Code for Biology and Medicine</i> , 2009, 4, 4.	1.7	1
84	The lifestyle of <i>Corynebacterium urealyticum</i> derived from its complete genome sequence established by pyrosequencing. <i>Journal of Biotechnology</i> , 2008, 136, 11-21.	3.8	81
85	Ultrafast pyrosequencing of <i>Corynebacterium kroppenstedtii</i> DSM44385 revealed insights into the physiology of a lipophilic corynebacterium that lacks mycolic acids. <i>Journal of Biotechnology</i> , 2008, 136, 22-30.	3.8	68
86	T-DNAâ€mediated transfer of <i>Agrobacterium tumefaciens</i> chromosomal DNA into plants. <i>Nature Biotechnology</i> , 2008, 26, 1015-1017.	17.5	64
87	MYBL2 is a new regulator of flavonoid biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2008, 55, 940-953.	5.7	474
88	AtMYB12 regulates caffeoyl quinic acid and flavonol synthesis in tomato: expression in fruit results in very high levels of both types of polyphenol. <i>Plant Journal</i> , 2008, 56, 316-326.	5.7	285
89	Genomeâ€scale <i>Arabidopsis</i> promoter array identifies targets of the histone acetyltransferase GCN5. <i>Plant Journal</i> , 2008, 56, 493-504.	5.7	120
90	A systematic survey in <i>Arabidopsis thaliana</i> of transcription factors that modulate circadian parameters. <i>BMC Genomics</i> , 2008, 9, 182.	2.8	58

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91	Construction and characterization of a sugar beet (<i>Beta vulgaris</i>) fosmid library. <i>Genome</i> , 2008, 51, 948-951.	2.0	25
92	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	3.8	238
93	Diversity of a Complex Centromeric Satellite and Molecular Characterization of Dispersed Sequence Families in Sugar Beet (<i>Beta vulgaris</i>). <i>Annals of Botany</i> , 2008, 102, 521-530.	2.9	25
94	GABI-Kat SimpleSearch: an <i>Arabidopsis thaliana</i> T-DNA mutant database with detailed information for confirmed insertions. <i>Nucleic Acids Research</i> , 2007, 35, D874-D878.	14.5	50
95	Differential regulation of closely related R2R3-MYB transcription factors controls flavonol accumulation in different parts of the <i>Arabidopsis thaliana</i> seedling. <i>Plant Journal</i> , 2007, 50, 660-677.	5.7	937
96	A simplified method for the analysis of transcription factor-promoter interactions that allows high-throughput data generation. <i>Plant Journal</i> , 2007, 50, 911-916.	5.7	47
97	The transcription factor HIG1/MYB51 regulates indolic glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2007, 50, 886-901.	5.7	371
98	Comparative sequence analysis of <i>Solanum</i> and <i>Arabidopsis</i> in a hot spot for pathogen resistance on potato chromosome V reveals a patchwork of conserved and rapidly evolving genome segments. <i>BMC Genomics</i> , 2007, 8, 112.	2.8	38
99	Analysis of DNA polymorphisms in sugar beet (<i>Beta vulgaris</i> L.) and development of an SNP-based map of expressed genes. <i>Theoretical and Applied Genetics</i> , 2007, 115, 601-615.	3.6	60
100	Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. <i>Planta</i> , 2007, 226, 147-158.	3.2	76
101	Iron deficiency-mediated stress regulation of four subgroup Ib BHLH genes in <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2007, 226, 897-908.	3.2	223
102	Analysis of T-DNA insertion site distribution patterns in <i>Arabidopsis thaliana</i> reveals special features of genes without insertions. <i>Genomics</i> , 2006, 87, 645-652.	2.9	38
103	Whole-Genome Sequence of <i>Listeria welshimeri</i> Reveals Common Steps in Genome Reduction with <i>Listeria innocua</i> as Compared to <i>Listeria monocytogenes</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7405-7415.	2.2	89
104	LucTrap Vectors Are Tools to Generate Luciferase Fusions for the Quantification of Transcript and Protein Abundance in Vivo. <i>Plant Physiology</i> , 2006, 141, 3-14.	4.8	31
105	Differential combinatorial interactions of cis-acting elements recognized by R2R3-MYB, BZIP, and BHLH factors control light-responsive and tissue-specific activation of phenylpropanoid biosynthesis genes. <i>Plant Molecular Biology</i> , 2005, 57, 155-171.	3.9	377
106	Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen <i>Corynebacterium jeikeium</i> K411, a Lipid-Requiring Bacterium of the Human Skin Flora. <i>Journal of Bacteriology</i> , 2005, 187, 4671-4682.	2.2	189
107	A Multilocus Sequence Survey in <i>Arabidopsis thaliana</i> Reveals a Genome-Wide Departure From a Neutral Model of DNA Sequence Polymorphism. <i>Genetics</i> , 2005, 169, 1601-1615.	2.9	188
108	The <i>Arabidopsis</i> Transcription Factor MYB12 Is a Flavonol-Specific Regulator of Phenylpropanoid Biosynthesis. <i>Plant Physiology</i> , 2005, 138, 1083-1096.	4.8	676

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109	TT2, TT8, and TTG1 synergistically specify the expression of BANYULS and proanthocyanidin biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 39, 366-380.	5.7	855
110	Comprehensive identification of <i>Arabidopsis thaliana</i> MYB transcription factors interacting with R/B-like BHLH proteins. <i>Plant Journal</i> , 2004, 40, 22-34.	5.7	773
111	FRU(BHLH029) is required for induction of iron mobilization genes in <i>Arabidopsis thaliana</i> . <i>FEBS Letters</i> , 2004, 577, 528-534.	2.8	325
112	An <i>Arabidopsis thaliana</i> T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics. <i>Plant Molecular Biology</i> , 2003, 53, 247-259.	3.9	666
113	Establishment of a high-efficiency SNP-based framework marker set for <i>Arabidopsis</i> . <i>Plant Journal</i> , 2003, 36, 122-140.	5.7	87
114	The Basic Helix-Loop-Helix Transcription Factor Family in Plants: A Genome-Wide Study of Protein Structure and Functional Diversity. <i>Molecular Biology and Evolution</i> , 2003, 20, 735-747.	8.9	913
115	Isolation and linkage analysis of expressed disease-resistance gene analogues of sugar beet (<i>Beta</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	2.0	54
116	Update on the Basic Helix-Loop-Helix Transcription Factor Gene Family in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2003, 15, 2497-2502.	6.6	282
117	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2003, 19, 1441-1442.	4.1	61
118	Large-Scale Identification and Analysis of Genome-Wide Single-Nucleotide Polymorphisms for Mapping in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2003, 13, 1250-1257.	5.5	184
119	High-throughput generation of sequence indexes from T-DNA mutagenized <i>Arabidopsis thaliana</i> lines. <i>BioTechniques</i> , 2003, 35, 1164-1168.	1.8	27
120	<i>A. thaliana</i> TRANSPARENT TESTA 1 is involved in seed coat development and defines the WIP subfamily of plant zinc finger proteins. <i>Genes and Development</i> , 2002, 16, 138-149.	5.9	180
121	bZIP transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2002, 7, 106-111.	8.8	1,585
122	REGIA, An EU Project on Functional Genomics of Transcription Factors from <i>Arabidopsis thaliana</i> . <i>Comparative and Functional Genomics</i> , 2002, 3, 102-108.	2.0	69
123	Construction of a "unigene"™ cDNA clone set by oligonucleotide fingerprinting allows access to 25,000 potential sugar beet genes. <i>Plant Journal</i> , 2002, 32, 845-857.	5.7	41
124	EST Sequencing, Annotation and Macroarray Transcriptome Analysis Identify Preferentially Root-Expressed Genes in Sugar Beet. <i>Plant Biology</i> , 2002, 4, 700-710.	3.8	23
125	SNP frequency and allelic haplotype structure of <i>Beta vulgaris</i> expressed genes. <i>Molecular Breeding</i> , 2001, 8, 63-74.	2.1	87
126	The R2R3-MYB gene family in <i>Arabidopsis thaliana</i> . <i>Current Opinion in Plant Biology</i> , 2001, 4, 447-456.	7.1	1,783

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127	Comparative Genomics and Regulatory Evolution: Conservation and Function of the Chs and Apetala3 Promoters. <i>Molecular Biology and Evolution</i> , 2001, 18, 1882-1891.	8.9	77
128	c-MYB oncogene-like genes encoding three MYB repeats occur in all major plant lineages. <i>Plant Journal</i> , 2000, 21, 231-235.	5.7	108
129	Transactivation properties of parsley proline-rich bZIP transcription factors. <i>Plant Journal</i> , 2000, 22, 1-8.	5.7	117
130	Transcriptional repression by AtMYB4 controls production of UV-protecting sunscreens in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2000, 19, 6150-6161.	7.8	797
131	Identification of the <i>Arabidopsis thaliana</i> Flavonoid 3'-Hydroxylase Gene and Functional Expression of the Encoded P450 Enzyme. <i>Biological Chemistry</i> , 2000, 381, 749-53.	2.5	205
132	Function Search in a Large Transcription Factor Gene Family in <i>Arabidopsis</i> : Assessing the Potential of Reverse Genetics to Identify Insertional Mutations in R2R3 MYB Genes. <i>Plant Cell</i> , 1999, 11, 1827-1840.	6.6	151
133	Characterization of tt15 , a novel transparent testa mutant of <i>Arabidopsis thaliana</i> (L.) Heynh.. <i>Planta</i> , 1999, 208, 352-357.	3.2	30
134	Function Search in a Large Transcription Factor Gene Family in <i>Arabidopsis</i> : Assessing the Potential of Reverse Genetics to Identify Insertional Mutations in R2R3 MYB Genes. <i>Plant Cell</i> , 1999, 11, 1827.	6.6	13
135	Identification of UV/blue light-response elements in the <i>Arabidopsis thaliana</i> chalcone synthase promoter using a homologous protoplast transient expression system. <i>Plant Molecular Biology</i> , 1998, 36, 741-754.	3.9	154
136	Phenylpropanoid biosynthesis and its regulation. <i>Current Opinion in Plant Biology</i> , 1998, 1, 251-257.	7.1	428
137	CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analyses of light-dependent expression, post-transcriptional regulation, nuclear import and heterodimerisation. <i>Molecular Genetics and Genomics</i> , 1998, 257, 595-605.	2.4	59
138	Towards functional characterisation of the members of the R2R3-MYB gene family from <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 1998, 16, 263-276.	5.7	554
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