

Bernd Weisshaar

List of Publications by Year in descending order

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161
papers

27,205
citations

13827

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docs citations

201
times ranked

20183
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#	ARTICLE	IF	CITATIONS
1	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. <i>BMC Genomics</i> , 2022, 23, 113.	1.2	10
2	Mapping-by-Sequencing Reveals Genomic Regions Associated with Seed Quality Parameters in <i>Brassica napus</i> . <i>Genes</i> , 2022, 13, 1131.	1.0	4
3	The transition to flowering in winter rapeseed during vernalization. <i>Plant, Cell and Environment</i> , 2021, 44, 506-518.	2.8	19
4	Reference-based QUantification Of gene Dispensability (QUOD). <i>Plant Methods</i> , 2021, 17, 18.	1.9	3
5	Transcriptomic analysis of temporal shifts in berry development between two grapevine cultivars of the Pinot family reveals potential genes controlling ripening time. <i>BMC Plant Biology</i> , 2021, 21, 327.	1.6	8
6	Large scale genomic rearrangements in selected <i>Arabidopsis thaliana</i> T-DNA lines are caused by T-DNA insertion mutagenesis. <i>BMC Genomics</i> , 2021, 22, 599.	1.2	42
7	Functional Characterisation of Banana (<i>Musa</i> spp.) 2-Oxoglutarate-Dependent Dioxygenases Involved in Flavonoid Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 701780.	1.7	20
8	A novel, robust and mating-competent <i>Chlamydomonas reinhardtii</i> strain with an enhanced transgene expression capacity for algal biotechnology. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 31, e00644.	2.1	10
9	Characterization of the <i>Brassica napus</i> Flavonol Synthase Gene Family Reveals Bifunctional Flavonol Synthases. <i>Frontiers in Plant Science</i> , 2021, 12, 733762.	1.7	24
10	Functional and evolutionary analysis of the <i>Arabidopsis</i> 4R-MYB protein SNAPc4 as part of the SNAP complex. <i>Plant Physiology</i> , 2021, 185, 1002-1020.	2.3	9
11	The R2R3-MYB gene family in banana (<i>Musa acuminata</i>): Genome-wide identification, classification and expression patterns. <i>PLoS ONE</i> , 2020, 15, e0239275.	1.1	39
12	RNA-Seq Time Series of <i>Vitis vinifera</i> Bud Development Reveals Correlation of Expression Patterns with the Local Temperature Profile. <i>Plants</i> , 2020, 9, 1548.	1.6	7
13	Genome Sequencing of <i>Musa acuminata</i> Dwarf Cavendish Reveals a Duplication of a Large Segment of Chromosome 2. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 37-42.	0.8	10
14	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar 'Bârner'™. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
15	High Contiguity de novo Genome Sequence Assembly of Trifoliate Yam (<i>Dioscorea dumetorum</i>) Using Long Read Sequencing. <i>Genes</i> , 2020, 11, 274.	1.0	54
16	A Partially Phase-Separated Genome Sequence Assembly of the <i>Vitis</i> Rootstock 'Bârner'™ (<i>Vitis riparia</i> × <i>Vitis rotundifolia</i>) Tj ETQq0 0 0 rgBT /Ove Science, 2020, 11, 156.	1.7	6
17	Characterization of genes and alleles involved in the control of flowering time in grapevine. <i>PLoS ONE</i> , 2019, 14, e0214703.	1.1	9
18	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the <i>Arabidopsis thaliana</i> Genome. <i>Genes</i> , 2019, 10, 671.	1.0	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.	1.1	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.	5.8	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.	0.6	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.	0.6	24
23	Evolution of tonoplast <i>P_{ATPase}</i> transporters involved in vacuolar acidification. <i>New Phytologist</i> , 2016, 211, 1092-1107.	3.5	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	1.8	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.	1.5	6
26	ReadXplorer 2 "detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016, 32, 3702-3708.	1.8	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.	0.4	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.	1.2	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.	2.8	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.	2.4	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.	1.1	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.	1.2	34
34	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184.	3.8	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.	1.2	56
36	TRANSPARENT TESTA 13 is a tonoplast <i>P_{3A}</i> <i>ATPase</i> required for vacuolar deposition of proanthocyanidins in <i>Arabidopsis thaliana</i> seeds. <i>Plant Journal</i> , 2015, 82, 840-849.	2.8	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.	3.9	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.	1.9	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.	1.6	95
40	Plant genome sequencing " applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	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.	2.8	17
42	Profiling of extensively diversified plant <sc>LINE</sc>s reveals distinct plant-specific subclades. <i>Plant Journal</i> , 2014, 79, 385-397.	2.8	35
43	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
44	The Genomics Revolution and its Impact on Future Biotechnology. <i>Journal of Biotechnology</i> , 2014, 190, 1.	1.9	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.	1.8	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.	1.6	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.	1.2	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.	1.1	18
49	Highly diverse chromoviruses of <i>Beta vulgaris</i> are classified by chromodomains and chromosomal integration. <i>Mobile DNA</i> , 2013, 4, 8.	1.3	36
50	<sc>GABI</sc>-<sc>DUPLO</sc>: a collection of double mutants to overcome genetic redundancy in <i>Arabidopsis thaliana</i>. <i>Plant Journal</i> , 2013, 75, 157-171.	2.8	48
51	Toward the identification and regulation of the <i>Arabidopsis thaliana</i> ABI3 regulon. <i>Nucleic Acids Research</i> , 2012, 40, 8240-8254.	6.5	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.	6.5	336
53	Evolutionary reshuffling in the Errantivirus lineage Elbe within the <i>Beta vulgaris</i> genome. <i>Plant Journal</i> , 2012, 72, 636-651.	2.8	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.	1.0	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.	1.8	135
56	Palaeohexaploid ancestry for Caryophyllales inferred from extensive gene-based physical and genetic mapping of the sugar beet genome (<i>Beta vulgaris</i>). <i>Plant Journal</i> , 2012, 70, 528-540.	2.8	58
57	Elongation-related functions of LEAFY COTYLEDON1 during the development of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2012, 71, 427-442.	2.8	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.	2.0	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.	0.1	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.	1.0	95
62	Two differentially expressed <i>MATE</i> factor genes from apple complement the <i>Arabidopsis</i> transparent testa2 mutant. <i>Plant Biology</i> , 2011, 13, 42-50.	1.8	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.	2.8	81
64	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
65	Epigenetic profiling of heterochromatic satellite DNA. <i>Chromosoma</i> , 2011, 120, 409-422.	1.0	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.	6.5	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.	3.1	116
68	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. <i>Theoretical and Applied Genetics</i> , 2010, 121, 549-565.	1.8	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.	2.8	78
70	Analysis of a c0t-1 library enables the targeted identification of minisatellite and satellite families in <i>Beta vulgaris</i> . <i>BMC Plant Biology</i> , 2010, 10, 8.	1.6	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.	0.6	48
72	Weird fingers: Functional analysis of WIP domain proteins. <i>FEBS Letters</i> , 2010, 584, 3116-3122.	1.3	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.	3.5	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.	2.8	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.	3.1	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.	1.0	23
77	MYB transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2010, 15, 573-581.	4.3	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.	6.5	139
79	The Grapevine R2R3-MYB Transcription Factor VvMYB1 Regulates Flavonol Synthesis in Developing Grape Berries. <i>Plant Physiology</i> , 2009, 151, 1513-1530.	2.3	383
80	<i>Arabidopsis thaliana</i> expresses a second functional flavonol synthase. <i>FEBS Letters</i> , 2009, 583, 1981-1986.	1.3	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.	1.6	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.	2.0	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.	1.9	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.	1.9	68
86	T-DNAâ€mediated transfer of <i>Agrobacterium tumefaciens</i> chromosomal DNA into plants. <i>Nature Biotechnology</i> , 2008, 26, 1015-1017.	9.4	64
87	MYBL2 is a new regulator of flavonoid biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2008, 55, 940-953.	2.8	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.	2.8	285
89	Genomeâ€scale <i>Arabidopsis</i> promoter array identifies targets of the histone acetyltransferase GCN5. <i>Plant Journal</i> , 2008, 56, 493-504.	2.8	120
90	A systematic survey in <i>Arabidopsis thaliana</i> of transcription factors that modulate circadian parameters. <i>BMC Genomics</i> , 2008, 9, 182.	1.2	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.	0.9	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.	1.9	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.	1.4	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.	6.5	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.	2.8	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.	2.8	47
97	The transcription factor HIG1/MYB51 regulates indolic glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2007, 50, 886-901.	2.8	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.	1.2	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.	1.8	60
100	Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. <i>Planta</i> , 2007, 226, 147-158.	1.6	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.	1.6	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.	1.3	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.	1.0	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.	2.3	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.	2.0	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.	1.0	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.	1.2	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.	2.3	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.	2.8	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.	2.8	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.	1.3	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.	2.0	666
113	Establishment of a high-efficiency SNP-based framework marker set for <i>Arabidopsis</i> . <i>Plant Journal</i> , 2003, 36, 122-140.	2.8	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.	3.5	913
115	Isolation and linkage analysis of expressed disease-resistance gene analogues of sugar beet (<i>Beta vulgaris</i>) Tj ETQq1 1 0.784314 rgBT/Overlook 0,9 54	0.9	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.	3.1	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.	1.8	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.	2.4	184
119	High-throughput generation of sequence indexes from T-DNA mutagenized <i>Arabidopsis thaliana</i> lines. <i>BioTechniques</i> , 2003, 35, 1164-1168.	0.8	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.	2.7	180
121	bZIP transcription factors in <i>Arabidopsis</i> . <i>Trends in Plant Science</i> , 2002, 7, 106-111.	4.3	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.	2.8	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.	1.8	23
125	SNP frequency and allelic haplotype structure of <i>Beta vulgaris</i> expressed genes. <i>Molecular Breeding</i> , 2001, 8, 63-74.	1.0	87
126	The R2R3-MYB gene family in <i>Arabidopsis thaliana</i> . <i>Current Opinion in Plant Biology</i> , 2001, 4, 447-456.	3.5	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.	3.5	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.	2.8	108
129	Transactivation properties of parsley proline-rich bZIP transcription factors. <i>Plant Journal</i> , 2000, 22, 1-8.	2.8	117
130	Transcriptional repression by AtMYB4 controls production of UV-protecting sunscreens in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2000, 19, 6150-6161.	3.5	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.	1.2	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.	3.1	151
133	Characterization of tt15 , a novel transparent testa mutant of <i>Arabidopsis thaliana</i> (L.) Heynh.. <i>Planta</i> , 1999, 208, 352-357.	1.6	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.	3.1	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.	2.0	154
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