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List of Publications by Year
in descending order

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162	3,065	186265	254184
papers	citations	28 h-index	43 g-index

164	164	164	3355
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification and characterization of carotenoid biosynthesis related genes in a novel dark skinned citrus mutant cultivar â€˜Suneatâ€™. Horticulture Environment and Biotechnology, 2021, 62, 99-111.	2.1	6
2	Glucosinolate profile and Myrosinase gene expression are modulated upon Plasmodiophora brassicae infection in cabbage. Functional Plant Biology, 2021, 48, 103.	2.1	4
3	Wholeâ€genome alignmentâ€based development of molecular markers for detecting Leptosphaeria maculans and Leptosphaeria biglobosa , the causal agents of blackleg disease in Brassicas. Journal of Phytopathology, 2021, 169, 283-294.	1.0	0
4	Inheritance of Black Rot Resistance and Development of Molecular Marker Linked to Xcc Races 6 and 7 Resistance in Cabbage. Plants, 2021, 10, 1940.	3.5	3
5	In silico analysis and expression profiling revealed Rlm1â€² blackleg disease-resistant genes in Chromosome 6 of Brassica oleracea. Horticulture Environment and Biotechnology, 2021, 62, 969-983.	2.1	1
6	Development of Molecular Markers for Specific Detection of Xanthomonas campestris pv. incanae. Plant Breeding and Biotechnology, 2021, 9, 287-297.	0.9	0
7	Molecular characterization of Acidovorax citrulli strain NIHHS15-280 causing bacterial fruit blotch disease in Korea and screening of resistance sources in melon. Horticulture Environment and Biotechnology, 2020, 61, 115-126.	2.1	8
8	Characterization of Insulin-Like Growth Factor Binding Protein 7 (Igfbp7) and Its Potential Involvement in Shell Formation and Metamorphosis of Pacific Abalone, Haliotis discus hannai. International Journal of Molecular Sciences, 2020, 21, 6529.	4.1	7
9	In silico characterization and expression of disease-resistance-related genes within the collinear region of Brassica napus blackleg resistant locus LepR1â€² in B. oleracea. Journal of General Plant Pathology, 2020, 86, 442-456.	1.0	4
10	Characterization, identification and expression profiling of genome-wide R-genes in melon and their putative roles in bacterial fruit blotch resistance. BMC Genetics, 2020, 21, 80.	2.7	7
11	ddRAD-seq derived genome-wide SNPs, high density linkage map and QTLs for fruit quality traits in strawberry (Fragaria x ananassa). 3 Biotech, 2020, 10, 353.	2.2	4
12	Expression and Role of Biosynthetic, Transporter, Receptor, and Responsive Genes for Auxin Signaling during Clubroot Disease Development. International Journal of Molecular Sciences, 2020, 21, 5554.	4.1	6
13	Transcriptome wide SSR discovery cross-taxa transferability and development of marker database for studying genetic diversity population structure of Lilium species. Scientific Reports, 2020, 10, 18621.	3.3	17
14	Leptosphaeria maculans Alters Glucosinolate Accumulation and Expression of Aliphatic and Indolic Glucosinolate Biosynthesis Genes in Blackleg Disease-Resistant and -Susceptible Cabbage Lines at the Seedling Stage. Frontiers in Plant Science, 2020, 11, 1134.	3.6	10
15	Knockout of SlMS10 Gene (Solyc02g079810) Encoding bHLH Transcription Factor Using CRISPR/Cas9 System Confers Male Sterility Phenotype in Tomato. Plants, 2020, 9, 1189.	3.5	21
16	In-silico identification and differential expression of putative disease resistance-related genes within the collinear region of Brassica napus blackleg resistance locus LepR2â€™ in Brassica oleracea. Horticulture Environment and Biotechnology, 2020, 61, 879-890.	2.1	8
17	Glucosinolate Profile and Glucosinolate Biosynthesis and Breakdown Gene Expression Manifested by Black Rot Disease Infection in Cabbage. Plants, 2020, 9, 1121.	3.5	10
18	Transcriptome Analysis by RNAâ€“Seq Reveals Genes Related to Plant Height in Two Sets of Parent-hybrid Combinations in Easter lily (Lilium longiflorum). Scientific Reports, 2020, 10, 9082.	3.3	19

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19	Expression and Role of Response Regulating, Biosynthetic and Degrading Genes for Cytokinin Signaling during Clubroot Disease Development. International Journal of Molecular Sciences, 2020, 21, 3896.	4.1	8
20	Development of powdery mildew race 5-specific SNP markers in Cucumis melo L. using whole-genome resequencing. Horticulture Environment and Biotechnology, 2020, 61, 347-357.	2.1	13
21	Development of Molecular Marker Linked with Bacterial Fruit Blotch Resistance in Melon (Cucumis) Tj ETQq1 1 0.784314 rgBT /Overlo	2.4	12
22	In-silico identification and differential expressions of LepR4-syntenic disease resistance related domain containing genes against blackleg causal fungus Leptosphaeria maculans in Brassica oleracea. Gene Reports, 2020, 19, 100598.	0.8	9
23	Molecular characterization and spatiotemporal expression of prohormone convertase 2 in the Pacific abalone, Haliotis discus hannai. PLoS ONE, 2020, 15, e0231353.	2.5	7
24	Development of diagnostic molecular markers for marker-assisted breeding against bacterial wilt in tomato. Breeding Science, 2020, 70, 462-473.	1.9	14
25	Development of PCR-Based Molecular Marker for Detection of Xanthomonas campestris pv. campestris Race 6, the Causative Agent of Black Rot of Brassicas. Plant Pathology Journal, 2020, 36, 418-427.	1.7	7
26	Title is missing!. , 2020, 15, e0231353.		0
27	Title is missing!. , 2020, 15, e0231353.		0
28	Title is missing!. , 2020, 15, e0231353.		0
29	Title is missing!. , 2020, 15, e0231353.		0
30	Title is missing!. , 2020, 15, e0231353.		0
31	Title is missing!. , 2020, 15, e0231353.		0
32	Abscisic acid and ethylene biosynthesis-related genes are associated with anthocyanin accumulation in purple ornamental cabbage (Brassica oleracea var. acephala). Genome, 2019, 62, 513-526.	2.0	10
33	Molecular Identification and Expression Analysis of Carbonic Anhydrase VII in Pufferfish (Takifugu) Tj ETQq1 1 0.784314 rgBT /Overlo	1.3	2
34	Development of a PCR test for detection of Xanthomonas campestris pv. raphani. Australasian Plant Pathology, 2019, 48, 179-182.	1.0	4
35	Development of Molecular Markers for Detection of Acidovorax citrulli Strains Causing Bacterial Fruit Blotch Disease in Melon. International Journal of Molecular Sciences, 2019, 20, 2715.	4.1	8
36	Molecular markers based on sequence variation in BoFLC1.C9 for characterizing early- and late-flowering cabbage genotypes. BMC Genetics, 2019, 20, 42.	2.7	21

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37	High density linkage map construction and QTL mapping for runner production in allo-octoploid strawberry Fragariaâ€‰Ã—â€‰ananassa based on ddRAD-seq derived SNPs. Scientific Reports, 2019, 9, 3275.	3.3	19
38	Genome-Wide Characterization of NBS-Encoding Genes in Watermelon and Their Potential Association with Gummy Stem Blight Resistance. International Journal of Molecular Sciences, 2019, 20, 902.	4.1	19
39	Molecular analysis of anthocyanin biosynthesis-related genes reveal BoTT8 associated with purple hypocotyl of broccoli (Brassica oleracea var. italica L.). Genome, 2019, 62, 253-266.	2.0	13
40	Inheritance Pattern and Molecular Markers for Resistance to Blackleg Disease in Cabbage. Plants, 2019, 8, 583.	3.5	9
41	Pathovar specific molecular detection of Xanthomonas campestris pv. campestris, the causal agent of black rot disease in cabbage. Canadian Journal of Plant Pathology, 2019, 41, 318-328.	1.4	7
42	Mapping of a novel clubroot resistance QTL using ddRAD-seq in Chinese cabbage (Brassica rapa L.). BMC Plant Biology, 2019, 19, 13.	3.6	55
43	Development of Molecular Marker through Genome Realignment for Specific Detection of Xanthomonas campestris pv. campestris Race 5, a Pathogen of Black Rot Disease. Journal of Microbiology and Biotechnology, 2019, 29, 785-793.	2.1	7
44	Role of Cytokinins in Clubroot Disease Development. Plant Breeding and Biotechnology, 2019, 7, 73-82.	0.9	8
45	Differential Expression Pattern of Lignin Biosynthetic Genes in Dwarf Cherry Tomato (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	2
46	Recurrent parent genome (RPG) recovery analysis in a marker-assisted backcross breeding based on the genotyping-by-sequencing in tomato (Solanum lycopersicum L.). Journal of Plant Biotechnology, 2019, 46, 165-171.	0.4	0
47	Expression of anthocyanin biosynthesis-related genes reflects the peel color in purple tomato. Horticulture Environment and Biotechnology, 2018, 59, 435-445.	2.1	14
48	Development of race-specific molecular marker forXanthomonas campestrispv.campestrisrace 3, the causal agent of black rot of crucifers. Canadian Journal of Plant Science, 2018, 98, 1119-1125.	0.9	12
49	Expression Profiling of the CSDP Transcription Factor Gene Family Points to Roles in Organ Development and Abiotic Stress Response in Tomato (Solanum lycopersicum L.). Plant Molecular Biology Reporter, 2018, 36, 273-283.	1.8	3
50	Molecular cloning and characterization of secretory carbonic anhydrase VI in pufferfish (Takifugu) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.2	3
51	Identification and Characterization of Anthocyanin Biosynthesis-Related Genes in Kohlrabi. Applied Biochemistry and Biotechnology, 2018, 184, 1120-1141.	2.9	24
52	Molecular analysis of anthocyanin-related genes in ornamental cabbage. Genome, 2018, 61, 111-120.	2.0	24
53	Transcriptome profiling of two contrasting ornamental cabbage (Brassica oleracea var. acephala) lines provides insights into purple and white inner leaf pigmentation. BMC Genomics, 2018, 19, 797.	2.8	27
54	Comparative transcriptome analysis provides insights into dwarfism in cherry tomato (Solanum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	2.5	7

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55	Glucosinolate Profiling and Expression Analysis of Glucosinolate Biosynthesis Genes Differentiate White Mold Resistant and Susceptible Cabbage Lines. International Journal of Molecular Sciences, 2018, 19, 4037.	4.1	21
56	Transcriptional regulation of anthocyanin biosynthesis in a high-anthocyanin resynthesized Brassica napus cultivar. Journal of Biological Research, 2018, 25, 19.	2.1	24
57	Developmental Stage and Shape of Embryo Determine the Efficacy of Embryo Rescue in Introgressing Orange/Yellow Color and Anthocyanin Genes of Brassica Species. Plants, 2018, 7, 99.	3.5	16
58	Altered Glucosinolate Profiles and Expression of Glucosinolate Biosynthesis Genes in Ringspot-Resistant and Susceptible Cabbage Lines. International Journal of Molecular Sciences, 2018, 19, 2833.	4.1	15
59	Varietal Identification of Open-Pollinated Onion Cultivars Using a Nanofluidic Array of Single Nucleotide Polymorphism (SNP) Markers. Agronomy, 2018, 8, 179.	3.0	2
60	Gummy Stem Blight Resistance in Melon: Inheritance Pattern and Development of Molecular Markers. International Journal of Molecular Sciences, 2018, 19, 2914.	4.1	19
61	Intronic Sequence Variations in a Gene with Peroxidase Domain Alter Bolting Time in Cabbage (Brassica) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	3
62	Molecular Cloning and Characterization of Carbonic Anhydrase XII from Pufferfish (Takifugu) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 T	4.1	0
63	Genome-Wide Identification, Characterization, and Expression Profiling of Glutathione S-Transferase (GST) Family in Pumpkin Reveals Likely Role in Cold-Stress Tolerance. Genes, 2018, 9, 84.	2.4	56
64	Exploration and Exploitation of Novel SSR Markers for Candidate Transcription Factor Genes in Lilium Species. Genes, 2018, 9, 97.	2.4	25
65	Purple Brassica oleracea var. capitata F. rubra is due to the loss of BoMYBL2â€“1 expression. BMC Plant Biology, 2018, 18, 82.	3.6	45
66	Expression Profiling of Regulatory and Biosynthetic Genes in Contrastingly Anthocyanin Rich Strawberry (Fragaria Ã— ananassa) Cultivars Reveals Key Genetic Determinants of Fruit Color. International Journal of Molecular Sciences, 2018, 19, 656.	4.1	26
67	SNP discovery of Korean short day onion inbred lines using double digest restriction site-associated DNA sequencing. PLoS ONE, 2018, 13, e0201229.	2.5	21
68	Whole-genome sequencing of Brassica oleracea var. capitata reveals new diversity of the mitogenome. PLoS ONE, 2018, 13, e0194356.	2.5	8
69	Identification of NBS-encoding genes linked to black rot resistance in cabbage (Brassica oleracea var.) Tj ETQq1 1 0.784314 rgBT /Overl	2.3	30
70	Screening of melon genotypes identifies gummy stem blight resistance associated with Gsb1 resistant loci. Journal of Plant Biotechnology, 2018, 45, 217-227.	0.4	8
71	Race- and Isolate-specific Molecular Marker Development through Genome-Realignment Enables Detection of Korean Plasmodiophora brassicae Isolates, Causal agents of Clubroot Disease. Plant Pathology Journal, 2018, 34, 506-513.	1.7	6
72	Screening of Cabbage (Brassica oleracea L.) Germplasm for Resistance to Black Rot. Plant Breeding and Biotechnology, 2018, 6, 30-43.	0.9	14

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73	LSAT: Liliaceae Simple Sequences Analysis Tool, a web server. Bioinformation, 2018, 14, 181-182.	0.5	4
74	Natural variation in CIRCADIAN CLOCK ASSOCIATED 1 is associated with flowering time in Brassica rapa. Genome, 2017, 60, 402-413.	2.0	4
75	Genome-wide expression profiling of aquaporin genes confer responses to abiotic and biotic stresses in Brassica rapa. BMC Plant Biology, 2017, 17, 23.	3.6	68
76	Molecular characterisation and expression profiling of calcineurin B-like (CBL) genes in Chinese cabbage under abiotic stresses. Functional Plant Biology, 2017, 44, 739.	2.1	10
77	A System for Distinguishing Octoploid Strawberry Cultivars Using High-Throughput SNP Genotyping. Tropical Plant Biology, 2017, 10, 68-76.	1.9	12
78	Korean Brassica oleracea germplasm offers a novel source of qualitative resistance to blackleg disease. European Journal of Plant Pathology, 2017, 149, 611-623.	1.7	16
79	Molecular breeding of a novel orange-brown tomato fruit with enhanced beta-carotene and chlorophyll accumulation. Hereditas, 2017, 154, 1.	1.4	24
80	Genome-wide characterization and stress-responsive expression profiling of MCM genes in Brassica oleracea and Brassica rapa. Journal of Plant Biology, 2017, 60, 472-484.	2.1	3
81	Discovery of candidate genes for heterosis breeding in Brassica oleracea L.. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	6
82	Differential Expression under Podosphaera xanthii and Abiotic Stresses Reveals Candidate MLO Family Genes in Cucumis melo L. Tropical Plant Biology, 2017, 10, 151-168.	1.9	3
83	New SNPs and InDel Variations in SlMYB12 Associated with Regulation of Pink Color in Tomato. Tropical Plant Biology, 2017, 10, 126-133.	1.9	4
84	Genome-wide analysis of gene expression to distinguish photoperiod-dependent and -independent flowering in Brassicaceae. Genes and Genomics, 2017, 39, 207-223.	1.4	2
85	Leptosphaeria maculans Alters Glucosinolate Profiles in Blackleg Diseaseâ€“Resistant and -Susceptible Cabbage Lines. Frontiers in Plant Science, 2017, 8, 1769.	3.6	19
86	Genome-wide analysis and expression profiling of zinc finger homeodomain (ZHD) family genes reveal likely roles in organ development and stress responses in tomato. BMC Genomics, 2017, 18, 695.	2.8	46
87	Whole-Genome Re-Alignment Facilitates Development of Specific Molecular Markers for Races 1 and 4 of Xanthomonas campestris pv. campestris, the Cause of Black Rot Disease in Brassica oleracea. International Journal of Molecular Sciences, 2017, 18, 2523.	4.1	17
88	Molecular Insights Reveal Psy1, SGR, and SlMYB12 Genes are Associated with Diverse Fruit Color Pigments in Tomato (Solanum lycopersicum L.). Molecules, 2017, 22, 2180.	3.8	21
89	Identification, Characterization and Expression Profiling of Stress-Related Genes in Easter Lily (Lilium) Tj ETQq1 1 0.784314 rgBT /Ove	2.4	10
90	Detection of Ribosomal DNA Sequence Polymorphisms in the Protist Plasmodiophora brassicae for the Identification of Geographical Isolates. International Journal of Molecular Sciences, 2017, 18, 84.	4.1	15

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91	Molecular Characterization and Expression Profiling of Tomato GRF Transcription Factor Family Genes in Response to Abiotic Stresses and Phytohormones. International Journal of Molecular Sciences, 2017, 18, 1056.	4.1	44
92	Reply to the Letter to the Editor by A. Schwelm and S. Neuhauser: â€œDetection of Ribosomal DNA Sequence Polymorphisms in the Protist Plasmodiophora brassicae for the Identification of Geographical Isolatesâ€• International Journal of Molecular Sciences, 2017, 18, 1455.	4.1	2
93	Genome-wide characterization and expression profiling of PDI family gene reveals function as abiotic and biotic stress tolerance in Chinese cabbage (Brassica rapa ssp. pekinensis). BMC Genomics, 2017, 18, 885.	2.8	48
94	SP-LL-37, human antimicrobial peptide, enhances disease resistance in transgenic rice. PLoS ONE, 2017, 12, e0172936.	2.5	12
95	Sugar content analysis and expression profiling of sugar related genes in contrasting Strawberry (Fragaria × ananassa) cultivars. Journal of Plant Biotechnology, 2017, 44, 178-190.	0.4	12
96	Genotyping-by-sequencing map permits identification of clubroot resistance QTLs and revision of the reference genome assembly in cabbage (Brassica oleraceaL.). DNA Research, 2016, 23, dsv034.	3.4	94
97	Genome-Wide Identification and Characterization of bZIP Transcription Factors inBrassica oleraceaunder Cold Stress. BioMed Research International, 2016, 2016, 1-18.	1.9	20
98	Glutathione Transferases Superfamily: Cold-Inducible Expression of Distinct GST Genes in Brassica oleracea. International Journal of Molecular Sciences, 2016, 17, 1211.	4.1	47
99	Genome-Wide Identification, Characterization and Expression Profiling of ADF Family Genes in Solanum lycopersicum L.. Genes, 2016, 7, 79.	2.4	20
100	Molecular and Functional Characterization of FLOWERING LOCUS T Homologs in Allium cepa. Molecules, 2016, 21, 217.	3.8	36
101	Exogenous Methyl Jasmonate and Salicylic Acid Induce Subspecies-Specific Patterns of Glucosinolate Accumulation and Gene Expression in Brassica oleracea L.. Molecules, 2016, 21, 1417.	3.8	54
102	Whole Genome Re-Sequencing and Characterization of Powdery Mildew Disease-Associated Allelic Variation in Melon. PLoS ONE, 2016, 11, e0157524.	2.5	32
103	De Novo Assembly and Transcriptome Analysis of Bulb Onion (Allium cepa L.) during Cold Acclimation Using Contrasting Genotypes. PLoS ONE, 2016, 11, e0161987.	2.5	28
104	A Genome-Wide Analysis Reveals Stress and Hormone Responsive Patterns of TIFY Family Genes in Brassica rapa. Frontiers in Plant Science, 2016, 7, 936.	3.6	41
105	Expression Profiling of Glucosinolate Biosynthetic Genes in Brassica oleracea L. var. capitata Inbred Lines Reveals Their Association with Glucosinolate Content. Molecules, 2016, 21, 787.	3.8	37
106	Sequence variation in SlMYB12 is associated with fruit peel color in pink tomato cultivars. Horticulture Environment and Biotechnology, 2016, 57, 274-279.	2.1	10
107	Genome-wide analysis of genes associated with bolting in heading type chinese cabbage. Euphytica, 2016, 212, 65-82.	1.2	5
108	Intracellular Ca2+ and K+ concentration in Brassica oleracea leaf induces differential expression of transporter and stress-related genes. BMC Genomics, 2016, 17, 211.	2.8	9

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109	Orange color is associated with CYC-B expression in tomato fleshy fruit. Molecular Breeding, 2016, 36, 1.	2.1	20
110	Identification and expression of a novel carbonic anhydrase isozyme in the pufferfish Takifugu vermicularis. Gene, 2016, 588, 173-179.	2.2	4
111	Expression of salicylic acid-related genes in Brassica oleracea var. capitata during Plasmodiophora brassicae infection. Genome, 2016, 59, 379-391.	2.0	23
112	Characterization and expression profiling of MYB transcription factors against stresses and during male organ development in Chinese cabbage (Brassica rapa ssp. pekinensis). Plant Physiology and Biochemistry, 2016, 104, 200-215.	5.8	29
113	Plant receptor kinases bind and phosphorylate 14-3-3 proteins. Genes and Genomics, 2016, 38, 1111-1119.	1.4	4
114	The complete chloroplast genome of Korean popular Citrus hybrid Hallabong mandarin [(Citrus unshiuÃ—C. sinensis)Ã—C. reticulate] (Rutaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 29-30.	0.4	2
115	Genome-wide identification, characterization and expression profiling of LIM family genes in Solanum lycopersicum L.. Plant Physiology and Biochemistry, 2016, 108, 177-190.	5.8	19
116	Gene loss/retention and evolutionary pattern of ascorbic acid biosynthesis and recycling genes in Brassica rapa following whole genome triplication. Genes and Genomics, 2016, 38, 1129-1143.	1.4	2
117	Identification of an SNP variation of elite tomato (Solanum lycopersicum L.) lines using genome resequencing analysis. Horticulture Environment and Biotechnology, 2016, 57, 173-181.	2.1	4
118	Alfin-like transcription factor family: characterization and expression profiling against stresses in Brassica oleracea. Acta Physiologiae Plantarum, 2016, 38, 1.	2.1	26
119	Genome-Wide Classification and Abiotic Stress-Responsive Expression Profiling of Carotenoid Oxygenase Genes in Brassica rapa and Brassica oleracea. Journal of Plant Growth Regulation, 2016, 35, 202-214.	5.1	24
120	Characterization and abiotic stress-responsive expression analysis ofSGT1genes inBrassica oleracea. Genome, 2016, 59, 243-251.	2.0	17
121	Whole genome de novo sequencing and genome annotation of the world popular cultivated edible mushroom, Lentinula edodes. Journal of Biotechnology, 2016, 223, 24-25.	3.8	55
122	GDSL esterase/lipase genes in Brassica rapa L.: genome-wide identification and expression analysis. Molecular Genetics and Genomics, 2016, 291, 531-542.	2.1	62
123	Developmental and Genotypic Variation in Leaf Wax Content and Composition, and in Expression of Wax Biosynthetic Genes in Brassica oleracea var. capitata. Frontiers in Plant Science, 2016, 7, 1972.	3.6	24
124	Identification and characterization ofS-RNasegenes in apple rootstock and the diversity ofS-RNasesinMalusspecies. Journal of Plant Biotechnology, 2016, 43, 49-57.	0.4	5
125	Identification of fungal races that cause powdery mildew in melon (Cucumis meloL.) and selection of resistant commercial melon cultivars against the identified races in Korea. Journal of Plant Biotechnology, 2016, 43, 58-65.	0.4	10
126	In vitroshoot regeneration and genetic transformation of the gerbera (Gerbera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Td (h	0.4	5

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127	Parentage Confirmation of Korean Bred Pear Cultivars by Simple Sequence Repeat SSR Genotyping and S-Genotypes Analysis. Plant Breeding and Biotechnology, 2016, 4, 198-211.	0.9	1
128	Functional analysis of the rice BRI1 receptor kinase. Journal of Plant Biotechnology, 2016, 43, 30-36.	0.4	0
129	Current status and prospects of plant diagnosis and phenomics research by using ICT remote sensing system. Journal of Plant Biotechnology, 2016, 43, 21-29.	0.4	0
130	Molecular Modeling of Myrosinase from Brassica oleracea: A Structural Investigation of Sinigrin Interaction. Genes, 2015, 6, 1315-1329.	2.4	8
131	Diversity and Inheritance of Intergenic Spacer Sequences of 45S Ribosomal DNA among Accessions of Brassica oleracea L. var. capitata. International Journal of Molecular Sciences, 2015, 16, 28783-28799.	4.1	13
132	Identification and Expression Analysis of Glucosinolate Biosynthetic Genes and Estimation of Glucosinolate Contents in Edible Organs of Brassica oleracea Subspecies. Molecules, 2015, 20, 13089-13111.	3.8	61
133	Functional analysis of the BRI1 receptor kinase by Thr-for-Ser substitution in a regulatory autophosphorylation site. Frontiers in Plant Science, 2015, 6, 562.	3.6	10
134	Suppression of ASKÎ² (AtSK32), a Clade III Arabidopsis GSK3, Leads to the Pollen Defect during Late Pollen Development. Molecules and Cells, 2015, 38, 506-517.	2.6	11
135	Identification and expression analysis of WRKY family genes under biotic and abiotic stresses in Brassica rapa. Molecular Genetics and Genomics, 2015, 290, 79-95.	2.1	62
136	Characterization and stress-induced expression analysis of Alfin-like transcription factors in Brassica rapa. Molecular Genetics and Genomics, 2015, 290, 1299-1311.	2.1	25
137	Molecular characterization of BZR transcription factor family and abiotic stress induced expression profiling in Brassica rapa. Plant Physiology and Biochemistry, 2015, 92, 92-104.	5.8	73
138	Molecular characterization of the UDP-glucose 4-epimerase (BrUGE) gene family in response to biotic and abiotic stress in Chinese cabbage (Brassica rapa). Plant Biotechnology Reports, 2015, 9, 339-350.	1.5	8
139	Genome-wide identification and characterization of MADS-box family genes related to organ development and stress resistance in Brassica rapa. BMC Genomics, 2015, 16, 178.	2.8	101
140	Anthocyanin biosynthesis for cold and freezing stress tolerance and desirable color in Brassica rapa. Functional and Integrative Genomics, 2015, 15, 383-394.	3.5	108
141	Response of NBS encoding resistance genes linked to both heat and fungal stress in Brassica oleracea. Plant Physiology and Biochemistry, 2015, 86, 130-136.	5.8	21
142	Identification and expression analysis of cold and freezing stress responsive genes of Brassica oleracea. Gene, 2015, 554, 215-223.	2.2	16
143	Global Gene-Expression Analysis to Identify Differentially Expressed Genes Critical for the Heat Stress Response in Brassica rapa. PLoS ONE, 2015, 10, e0130451.	2.5	44
144	Development of molecular marker to select resistant lines and to differentiate the races related to powdery mildew in melon (Cucumis meloL.). Journal of Plant Biotechnology, 2015, 42, 284-289.	0.4	8

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145	Genome-Wide Comparative Analysis of 20 Miniature Inverted-Repeat Transposable Element Families in Brassica rapa and B. oleracea. PLoS ONE, 2014, 9, e94499.	2.5	38
146	Identification and characterization of LIM gene family in Brassica rapa. BMC Genomics, 2014, 15, 641.	2.8	19
147	Genome-wide analysis of the distribution of AP2/ERF transcription factors reveals duplication and CBFs genes elucidate their potential function in Brassica oleracea. BMC Genomics, 2014, 15, 422.	2.8	47
148	Identification of Yellow Pigmentation Genes inBrassica rapassp.pekinensisUsing Br300 Microarray. International Journal of Genomics, 2014, 2014, 1-11.	1.6	5
149	Comparative transcriptome profiling of freezing stress responsiveness in two contrasting Chinese cabbage genotypes, Chiifu and Kenshin. Genes and Genomics, 2014, 36, 215-227.	1.4	10
150	Transcriptome analysis of newly classified bZIP transcription factors of Brassica rapa in cold stress response. Genomics, 2014, 104, 194-202.	2.9	37
151	Characterization of dihydroflavonol 4-reductase (DFR) genes and their association with cold and freezing stress in Brassica rapa. Gene, 2014, 550, 46-55.	2.2	96
152	Characterization of self-incompatibility genes in the intergeneric hybrid xBrassicoraphanus. Plant Systematics and Evolution, 2014, 300, 1903-1911.	0.9	3
153	Genome-Wide Transcriptome Analysis of Two Contrasting Brassica rapa Doubled Haploid Lines under Cold-Stresses Using Br135K Oligomeric Chip. PLoS ONE, 2014, 9, e106069.	2.5	24
154	Genome-wide expression profiles of contrasting inbred lines of Chinese cabbage, Chiifu and Kenshin, under temperature stress. Genes and Genomics, 2013, 35, 273-288.	1.4	20
155	Enhancement of resistance to soft rot (Pectobacterium carotovorum subsp. carotovorum) in transgenic Brassica rapa. European Journal of Plant Pathology, 2013, 136, 317-322.	1.7	2
156	Molecular characterization of thaumatin family genes related to stresses in Brassica rapa. Scientia Horticulturae, 2013, 152, 26-34.	3.6	24
157	Characterization and expression analysis of dirigent family genes related to stresses in Brassica. Plant Physiology and Biochemistry, 2013, 67, 144-153.	5.8	56
158	Identification and characterization of stress resistance related genes of Brassica rapa. Biotechnology Letters, 2012, 34, 979-987.	2.2	24
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