

# Ill-Sup Nou

## List of Publications by Year in descending order

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citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Genotyping-by-sequencing map permits identification of clubroot resistance QTLs and revision of the reference genome assembly in cabbage ( <i>Brassica oleracea</i> L.). DNA Research, 2016, 23, dsv034.	3.4	94
5	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
6	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
7	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
8	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
9	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
10	Characterization and expression analysis of dirigent family genes related to stresses in Brassica. Plant Physiology and Biochemistry, 2013, 67, 144-153.	5.8	56
11	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
12	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
13	Mapping of a novel clubroot resistance QTL using ddRAD-seq in Chinese cabbage ( <i>Brassica rapa</i> L.). BMC Plant Biology, 2019, 19, 13.	3.6	55
14	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
15	Genome-wide characterization and expression profiling of PDI family gene reveals function as abiotic and biotic stress tolerance in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). BMC Genomics, 2017, 18, 885.	2.8	48
16	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
17	Glutathione Transferases Superfamily: Cold-Inducible Expression of Distinct GST Genes in Brassica oleracea. International Journal of Molecular Sciences, 2016, 17, 1211.	4.1	47
18	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

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19	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
20	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
21	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
22	Identification and expression analysis of chitinase genes related to biotic stress resistance in Brassica. Molecular Biology Reports, 2012, 39, 3649-3657.	2.3	42
23	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
24	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
25	Transcriptome analysis of newly classified bZIP transcription factors of Brassica rapa in cold stress response. Genomics, 2014, 104, 194-202.	2.9	37
26	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
27	Molecular and Functional Characterization of FLOWERING LOCUS T Homologs in Allium cepa. Molecules, 2016, 21, 217.	3.8	36
28	Whole Genome Re-Sequencing and Characterization of Powdery Mildew Disease-Associated Allelic Variation in Melon. PLoS ONE, 2016, 11, e0157524.	2.5	32
29	Identification of NBS-encoding genes linked to black rot resistance in cabbage (Brassica oleracea var.) Tj ETQq1 1 0,784314 rgBT /Over	2.3	30
30	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
31	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
32	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
33	Alfin-like transcription factor family: characterization and expression profiling against stresses in Brassica oleracea. Acta Physiologiae Plantarum, 2016, 38, 1.	2.1	26
34	Expression Profiling of Regulatory and Biosynthetic Genes in Contrastingly Anthocyanin Rich Strawberry (Fragaria Å— ananassa) Cultivars Reveals Key Genetic Determinants of Fruit Color. International Journal of Molecular Sciences, 2018, 19, 656.	4.1	26
35	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
36	Exploration and Exploitation of Novel SSR Markers for Candidate Transcription Factor Genes in Lilium Species. Genes, 2018, 9, 97.	2.4	25

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37	Identification and characterization of stress resistance related genes of Brassica rapa. Biotechnology Letters, 2012, 34, 979-987.	2.2	24
38	Molecular characterization of thaumatin family genes related to stresses in Brassica rapa. Scientia Horticulturae, 2013, 152, 26-34.	3.6	24
39	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
40	Molecular breeding of a novel orange-brown tomato fruit with enhanced beta-carotene and chlorophyll accumulation. Hereditas, 2017, 154, 1.	1.4	24
41	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
42	Identification and Characterization of Anthocyanin Biosynthesis-Related Genes in Kohlrabi. Applied Biochemistry and Biotechnology, 2018, 184, 1120-1141.	2.9	24
43	Molecular analysis of anthocyanin-related genes in ornamental cabbage. Genome, 2018, 61, 111-120.	2.0	24
44	Transcriptional regulation of anthocyanin biosynthesis in a high-anthocyanin resynthesized Brassica napus cultivar. Journal of Biological Research, 2018, 25, 19.	2.1	24
45	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
46	Expression of salicylic acid-related genes in Brassica oleracea var. capitata during Plasmodiophora brassicae infection. Genome, 2016, 59, 379-391.	2.0	23
47	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
48	Molecular Insights Reveal Psy1, SGR, and SIMYB12 Genes are Associated with Diverse Fruit Color Pigments in Tomato (Solanum lycopersicum L.). Molecules, 2017, 22, 2180.	3.8	21
49	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
50	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
51	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
52	Knockout of SIMS10 Gene (Solyc02g079810) Encoding bHLH Transcription Factor Using CRISPR/Cas9 System Confers Male Sterility Phenotype in Tomato. Plants, 2020, 9, 1189.	3.5	21
53	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
54	Genome-Wide Identification and Characterization of bZIP Transcription Factors in Brassica oleracea under Cold Stress. BioMed Research International, 2016, 2016, 1-18.	1.9	20

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55	Genome-Wide Identification, Characterization and Expression Profiling of ADF Family Genes in <i>Solanum lycopersicum</i> L.. <i>Genes</i> , 2016, 7, 79.	2.4	20
56	Orange color is associated with CYC-B expression in tomato fleshy fruit. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	20
57	Identification and characterization of LIM gene family in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2014, 15, 641.	2.8	19
58	Genome-wide identification, characterization and expression profiling of LIM family genes in <i>Solanum lycopersicum</i> L.. <i>Plant Physiology and Biochemistry</i> , 2016, 108, 177-190.	5.8	19
59	<i>Leptosphaeria maculans</i> Alters Glucosinolate Profiles in Blackleg Disease-Resistant and -Susceptible Cabbage Lines. <i>Frontiers in Plant Science</i> , 2017, 8, 1769.	3.6	19
60	Gummy Stem Blight Resistance in Melon: Inheritance Pattern and Development of Molecular Markers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2914.	4.1	19
61	High density linkage map construction and QTL mapping for runner production in allo-octoploid strawberry <i>Fragaria</i> – <i>Ananassa</i> based on ddRAD-seq derived SNPs. <i>Scientific Reports</i> , 2019, 9, 3275.	3.3	19
62	Genome-Wide Characterization of NBS-Encoding Genes in Watermelon and Their Potential Association with Gummy Stem Blight Resistance. <i>International Journal of Molecular Sciences</i> , 2019, 20, 902.	4.1	19
63	Transcriptome Analysis by RNA-Seq Reveals Genes Related to Plant Height in Two Sets of Parent-hybrid Combinations in Easter lily ( <i>Lilium longiflorum</i> ). <i>Scientific Reports</i> , 2020, 10, 9082.	3.3	19
64	Characterization and abiotic stress-responsive expression analysis of <i>SGT1</i> genes in <i>Brassica oleracea</i> . <i>Genome</i> , 2016, 59, 243-251.	2.0	17
65	Whole-Genome Re-Alignment Facilitates Development of Specific Molecular Markers for Races 1 and 4 of <i>Xanthomonas campestris</i> pv. <i>campestris</i> , the Cause of Black Rot Disease in <i>Brassica oleracea</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 2523.	4.1	17
66	Transcriptome wide SSR discovery cross-taxa transferability and development of marker database for studying genetic diversity population structure of <i>Lilium</i> species. <i>Scientific Reports</i> , 2020, 10, 18621.	3.3	17
67	Determination of self-incompatibility genotypes of Korean apple cultivars based on S-RNase PCR. <i>Journal of Plant Biology</i> , 2006, 49, 448-454.	2.1	16
68	Identification and expression analysis of cold and freezing stress responsive genes of <i>Brassica oleracea</i> . <i>Gene</i> , 2015, 554, 215-223.	2.2	16
69	Korean <i>Brassica oleracea</i> germplasm offers a novel source of qualitative resistance to blackleg disease. <i>European Journal of Plant Pathology</i> , 2017, 149, 611-623.	1.7	16
70	Developmental Stage and Shape of Embryo Determine the Efficacy of Embryo Rescue in Introgressing Orange/Yellow Color and Anthocyanin Genes of <i>Brassica</i> Species. <i>Plants</i> , 2018, 7, 99.	3.5	16
71	Detection of Ribosomal DNA Sequence Polymorphisms in the Protist <i>Plasmodiophora brassicae</i> for the Identification of Geographical Isolates. <i>International Journal of Molecular Sciences</i> , 2017, 18, 84.	4.1	15
72	Altered Glucosinolate Profiles and Expression of Glucosinolate Biosynthesis Genes in Ringspot-Resistant and Susceptible Cabbage Lines. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2833.	4.1	15

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73	Expression of anthocyanin biosynthesis-related genes reflects the peel color in purple tomato. Horticulture Environment and Biotechnology, 2018, 59, 435-445.	2.1	14
74	Screening of Cabbage ( <i>Brassica oleracea</i> L.) Germplasm for Resistance to Black Rot. Plant Breeding and Biotechnology, 2018, 6, 30-43.	0.9	14
75	Development of diagnostic molecular markers for marker-assisted breeding against bacterial wilt in tomato. Breeding Science, 2020, 70, 462-473.	1.9	14
76	Diversity and Inheritance of Intergenic Spacer Sequences of 45S Ribosomal DNA among Accessions of <i>Brassica oleracea</i> L. var. capitata. International Journal of Molecular Sciences, 2015, 16, 28783-28799.	4.1	13
77	Molecular analysis of anthocyanin biosynthesis-related genes reveal BoTT8 associated with purple hypocotyl of broccoli ( <i>Brassica oleracea</i> var. italica L.). Genome, 2019, 62, 253-266.	2.0	13
78	Development of powdery mildew race 5-specific SNP markers in <i>Cucumis melo</i> L. using whole-genome resequencing. Horticulture Environment and Biotechnology, 2020, 61, 347-357.	2.1	13
79	A System for Distinguishing Octoploid Strawberry Cultivars Using High-Throughput SNP Genotyping. Tropical Plant Biology, 2017, 10, 68-76.	1.9	12
80	Development of race-specific molecular marker for <i>Xanthomonas campestris</i> pv. <i>campestris</i> race 3, the causal agent of black rot of crucifers. Canadian Journal of Plant Science, 2018, 98, 1119-1125.	0.9	12
81	Development of Molecular Marker Linked with Bacterial Fruit Blotch Resistance in Melon ( <i>Cucumis</i> ) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf	2.4	12
82	SP-LL-37, human antimicrobial peptide, enhances disease resistance in transgenic rice. PLoS ONE, 2017, 12, e0172936.	2.5	12
83	Sugar content analysis and expression profiling of sugar related genes in contrasting Strawberry ( <i>Fragaria</i> & <i>ananassa</i> ) cultivars. Journal of Plant Biotechnology, 2017, 44, 178-190.	0.4	12
84	The Presence of a New S-RNase Allele (S10) in Asian Pear ( <i>Pyrus pyrifolia</i> (Burm; Nakai)). Genetic Resources and Crop Evolution, 2006, 53, 1375-1383.	1.6	11
85	Suppression of ASK1 <sup>2</sup> (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
86	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
87	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
88	Sequence variation in SIMYB12 is associated with fruit peel color in pink tomato cultivars. Horticulture Environment and Biotechnology, 2016, 57, 274-279.	2.1	10
89	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
90	Identification, Characterization and Expression Profiling of Stress-Related Genes in Easter Lily ( <i>Lilium</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf	2.4	10

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91	Abscisic acid and ethylene biosynthesis-related genes are associated with anthocyanin accumulation in purple ornamental cabbage ( <i>Brassica oleracea</i> var. <i>acephala</i> ). <i>Genome</i> , 2019, 62, 513-526.	2.0	10
92	<i>Leptosphaeria maculans</i> Alters Glucosinolate Accumulation and Expression of Aliphatic and Indolic Glucosinolate Biosynthesis Genes in Blackleg Disease-Resistant and -Susceptible Cabbage Lines at the Seedling Stage. <i>Frontiers in Plant Science</i> , 2020, 11, 1134.	3.6	10
93	Glucosinolate Profile and Glucosinolate Biosynthesis and Breakdown Gene Expression Manifested by Black Rot Disease Infection in Cabbage. <i>Plants</i> , 2020, 9, 1121.	3.5	10
94	Identification of fungal races that cause powdery mildew in melon ( <i>Cucumis melo</i> L.) and selection of resistant commercial melon cultivars against the identified races in Korea. <i>Journal of Plant Biotechnology</i> , 2016, 43, 58-65.	0.4	10
95	Intracellular Ca <sup>2+</sup> and K <sup>+</sup> concentration in <i>Brassica oleracea</i> leaf induces differential expression of transporter and stress-related genes. <i>BMC Genomics</i> , 2016, 17, 211.	2.8	9
96	Inheritance Pattern and Molecular Markers for Resistance to Blackleg Disease in Cabbage. <i>Plants</i> , 2019, 8, 583.	3.5	9
97	In-silico identification and differential expressions of LepR4-syntenic disease resistance related domain containing genes against blackleg causal fungus <i>Leptosphaeria maculans</i> in <i>Brassica oleracea</i> . <i>Gene Reports</i> , 2020, 19, 100598.	0.8	9
98	Development of Self-Compatible <i>B. rapa</i> by RNAi-Mediated S Locus Gene Silencing. <i>PLoS ONE</i> , 2012, 7, e49497.	2.5	9
99	Molecular Modeling of Myrosinase from <i>Brassica oleracea</i> : A Structural Investigation of Sinigrin Interaction. <i>Genes</i> , 2015, 6, 1315-1329.	2.4	8
100	Molecular characterization of the UDP-glucose 4-epimerase (BrUGE) gene family in response to biotic and abiotic stress in Chinese cabbage ( <i>Brassica rapa</i> ). <i>Plant Biotechnology Reports</i> , 2015, 9, 339-350.	1.5	8
101	Whole-genome sequencing of <i>Brassica oleracea</i> var. <i>capitata</i> reveals new diversity of the mitogenome. <i>PLoS ONE</i> , 2018, 13, e0194356.	2.5	8
102	Development of Molecular Markers for Detection of <i>Acidovorax citrulli</i> Strains Causing Bacterial Fruit Blotch Disease in Melon. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2715.	4.1	8
103	Molecular characterization of <i>Acidovorax citrulli</i> strain NIHHS15-280 causing bacterial fruit blotch disease in Korea and screening of resistance sources in melon. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 115-126.	2.1	8
104	In-silico identification and differential expression of putative disease resistance-related genes within the collinear region of <i>Brassica napus</i> blackleg resistance locus LepR2™ in <i>Brassica oleracea</i> . <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 879-890.	2.1	8
105	Expression and Role of Response Regulating, Biosynthetic and Degrading Genes for Cytokinin Signaling during Clubroot Disease Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3896.	4.1	8
106	Development of molecular marker to select resistant lines and to differentiate the races related to powdery mildew in melon ( <i>Cucumis melo</i> L.). <i>Journal of Plant Biotechnology</i> , 2015, 42, 284-289.	0.4	8
107	Screening of melon genotypes identifies gummy stem blight resistance associated with <i>Gsb1</i> resistant loci. <i>Journal of Plant Biotechnology</i> , 2018, 45, 217-227.	0.4	8
108	Role of Cytokinins in Clubroot Disease Development. <i>Plant Breeding and Biotechnology</i> , 2019, 7, 73-82.	0.9	8



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109	Comparative transcriptome analysis provides insights into dwarfism in cherry tomato ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.5	7
110	Pathovar specific molecular detection of <i>Xanthomonas campestris</i> pv. <i>campestris</i> , the causal agent of black rot disease in cabbage. Canadian Journal of Plant Pathology, 2019, 41, 318-328.	1.4	7
111	Characterization of Insulin-Like Growth Factor Binding Protein 7 (Igfbp7) and Its Potential Involvement in Shell Formation and Metamorphosis of Pacific Abalone, <i>Haliotis discus hannai</i> . International Journal of Molecular Sciences, 2020, 21, 6529.	4.1	7
112	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
113	Molecular characterization and spatiotemporal expression of prohormone convertase 2 in the Pacific abalone, <i>Haliotis discus hannai</i> . PLoS ONE, 2020, 15, e0231353.	2.5	7
114	Development of Molecular Marker through Genome Realignment for Specific Detection of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Race 5, a Pathogen of Black Rot Disease. Journal of Microbiology and Biotechnology, 2019, 29, 785-793.	2.1	7
115	Development of PCR-Based Molecular Marker for Detection of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Race 6, the Causative Agent of Black Rot of Brassicas. Plant Pathology Journal, 2020, 36, 418-427.	1.7	7
116	Discovery of candidate genes for heterosis breeding in <i>Brassica oleracea</i> L.. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	6
117	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
118	Identification and characterization of carotenoid biosynthesis related genes in a novel dark skinned citrus mutant cultivar 'Suneat'™. Horticulture Environment and Biotechnology, 2021, 62, 99-111.	2.1	6
119	Race- and Isolate-specific Molecular Marker Development through Genome-Realignment Enables Detection of Korean <i>Plasmodiophora brassicae</i> Isolates, Causal agents of Clubroot Disease. Plant Pathology Journal, 2018, 34, 506-513.	1.7	6
120	Identification of Yellow Pigmentation Genes in <i>Brassica rapa</i> ssp. <i>pekinensis</i> Using Br300 Microarray. International Journal of Genomics, 2014, 2014, 1-11.	1.6	5
121	Genome-wide analysis of genes associated with bolting in heading type chinese cabbage. Euphytica, 2016, 212, 65-82.	1.2	5
122	Identification and characterization of <i>S-RNase</i> genes in apple rootstock and the diversity of <i>S-RNases</i> in <i>Malus</i> species. Journal of Plant Biotechnology, 2016, 43, 49-57.	0.4	5
123	<i>In vitro</i> shoot regeneration and genetic transformation of the gerbera ( <i>Gerbera</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.4	5
124	Identification and expression of a novel carbonic anhydrase isozyme in the pufferfish <i>Takifugu vermicularis</i> . Gene, 2016, 588, 173-179.	2.2	4
125	Plant receptor kinases bind and phosphorylate 14-3-3 proteins. Genes and Genomics, 2016, 38, 1111-1119.	1.4	4
126	Identification of an SNP variation of elite tomato ( <i>Solanum lycopersicum</i> L.) lines using genome resequencing analysis. Horticulture Environment and Biotechnology, 2016, 57, 173-181.	2.1	4



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127	Natural variation in <i>CIRCADIAN CLOCK ASSOCIATED 1</i> is associated with flowering time in <i>Brassica rapa</i> . <i>Genome</i> , 2017, 60, 402-413.	2.0	4
128	New SNPs and InDel Variations in <i>SLMYB12</i> Associated with Regulation of Pink Color in Tomato. <i>Tropical Plant Biology</i> , 2017, 10, 126-133.	1.9	4
129	Development of a PCR test for detection of <i>Xanthomonas campestris</i> pv. <i>raphani</i> . <i>Australasian Plant Pathology</i> , 2019, 48, 179-182.	1.0	4
130	In silico characterization and expression of disease-resistance-related genes within the collinear region of <i>Brassica napus</i> blackleg resistant locus <i>LepR1</i> in <i>B. oleracea</i> . <i>Journal of General Plant Pathology</i> , 2020, 86, 442-456.	1.0	4
131	ddRAD-seq derived genome-wide SNPs, high density linkage map and QTLs for fruit quality traits in strawberry ( <i>Fragaria x ananassa</i> ). <i>3 Biotech</i> , 2020, 10, 353.	2.2	4
132	Glucosinolate profile and Myrosinase gene expression are modulated upon <i>Plasmodiophora brassicae</i> infection in cabbage. <i>Functional Plant Biology</i> , 2021, 48, 103.	2.1	4
133	LSAT: Liliaceae Simple Sequences Analysis Tool, a web server. <i>Bioinformatics</i> , 2018, 14, 181-182.	0.5	4
134	Characterization of self-incompatibility genes in the intergeneric hybrid <i>xBrassicoraphanus</i> . <i>Plant Systematics and Evolution</i> , 2014, 300, 1903-1911.	0.9	3
135	Genome-wide characterization and stress-responsive expression profiling of MCM genes in <i>Brassica oleracea</i> and <i>Brassica rapa</i> . <i>Journal of Plant Biology</i> , 2017, 60, 472-484.	2.1	3
136	Differential Expression under <i>Podosphaera xanthii</i> and Abiotic Stresses Reveals Candidate MLO Family Genes in <i>Cucumis melo</i> L. <i>Tropical Plant Biology</i> , 2017, 10, 151-168.	1.9	3
137	Expression Profiling of the CSDP Transcription Factor Gene Family Points to Roles in Organ Development and Abiotic Stress Response in Tomato ( <i>Solanum lycopersicum</i> L.). <i>Plant Molecular Biology Reporter</i> , 2018, 36, 273-283.	1.8	3
138	Molecular cloning and characterization of secretory carbonic anhydrase VI in pufferfish ( <i>Takifugu</i> ). <i>Overlook 10 Tf 2000</i>	2.2	3
139	Intronic Sequence Variations in a Gene with Peroxidase Domain Alter Bolting Time in Cabbage ( <i>Brassica</i> ). <i>Overlook 10 Tf 2000</i>	1.8	3
140	Inheritance of Black Rot Resistance and Development of Molecular Marker Linked to Xcc Races 6 and 7 Resistance in Cabbage. <i>Plants</i> , 2021, 10, 1940.	3.5	3
141	Enhancement of resistance to soft rot ( <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> ) in transgenic <i>Brassica rapa</i> . <i>European Journal of Plant Pathology</i> , 2013, 136, 317-322.	1.7	2
142	The complete chloroplast genome of Korean popular <i>Citrus</i> hybrid Hallabong mandarin [( <i>Citrus unshiu</i> × <i>C. sinensis</i> ) × <i>C. reticulata</i> ] (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 29-30.	0.4	2
143	Gene loss/retention and evolutionary pattern of ascorbic acid biosynthesis and recycling genes in <i>Brassica rapa</i> following whole genome triplication. <i>Genes and Genomics</i> , 2016, 38, 1129-1143.	1.4	2
144	Genome-wide analysis of gene expression to distinguish photoperiod-dependent and -independent flowering in Brassicaceae. <i>Genes and Genomics</i> , 2017, 39, 207-223.	1.4	2

#	ARTICLE	IF	CITATIONS
145	Reply to the Letter to the Editor by A. Schwelm and S. Neuhauser: "Detection of Ribosomal DNA Sequence Polymorphisms in the Protist Plasmodiophora brassicae for the Identification of Geographical Isolates". International Journal of Molecular Sciences, 2017, 18, 1455.	4.1	2
146	Varietal Identification of Open-Pollinated Onion Cultivars Using a Nanofluidic Array of Single Nucleotide Polymorphism (SNP) Markers. Agronomy, 2018, 8, 179.	3.0	2
147	Molecular Identification and Expression Analysis of Carbonic Anhydrase VII in Pufferfish (Takifugu) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlock 10 Tf 50 62	1.3	0
148	Differential Expression Pattern of Lignin Biosynthetic Genes in Dwarf Cherry Tomato (Solanum) Tj ETQq0 0 0 rgBT <sub>0</sub> /Overlock 10 Tf 50 62	0.9	2
149	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
150	In silico analysis and expression profiling revealed Rlm1 <sup>Δ</sup> blackleg disease-resistant genes in Chromosome 6 of Brassica oleracea. Horticulture Environment and Biotechnology, 2021, 62, 969-983.	2.1	1
151	Molecular Cloning and Characterization of Carbonic Anhydrase XII from Pufferfish (Takifugu) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlock 10 Tf 50 62	4.1	0
152	Whole-genome alignment-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
153	Functional analysis of the rice BRI1 receptor kinase. Journal of Plant Biotechnology, 2016, 43, 30-36.	0.4	0
154	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
155	Recurrent parent genome (RPG) recovery analysis in a marker-assisted backcross breeding based on the genotyping-by-sequencing in tomato (<i>Solanum lycopersicum L.</i>). Journal of Plant Biotechnology, 2019, 46, 165-171.	0.4	0
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