Wenran Wang

List of Publications by Year
in descending order

55 papers	1,945 citations	218677 26 h-index	254184 43 g-index
55 all docs	55 docs citations	55 times ranked	1999 citing authors

#	Article	IF	Citations
1	Flexible Capacitive Pressure Sensor Based on Microstructured Composite Dielectric Layer for Broad Linear Range Pressure Sensing Applications. Micromachines, 2022, 13, 223.	2.9	17
2	Genetic and Molecular Regulation Mechanisms in the Formation and Development of Vegetable Fruit Shape. Applied Sciences (Switzerland), 2022, 12, 1514.	2.5	4
3	Characterization and regulatory mechanism analysis of VvmiR156aâ€" <i>VvAGL80</i> pair during grapevine flowering and parthenocarpy process induced by gibberellin. Plant Genome, 2022, 15, e20181.	2.8	2
4	Multilayer Flexible Pressure Sensor With High Sensitivity Over Wide Linearity Detection Range (August 2021). IEEE Transactions on Instrumentation and Measurement, 2021, 70, 1-9.	4.7	7
5	The role of <i>VvMYBA2r</i> and <i>VvMYBA2w</i> alleles of the <i>MYBA2</i> locus in the regulation of anthocyanin biosynthesis for molecular breeding of grape (<i>Vitis</i> spp.) skin coloration. Plant Biotechnology Journal, 2021, 19, 1216-1239.	8.3	39
6	Characterization and Action Mechanism Analysis of VvmiR156b/c/d-VvSPL9 Module Responding to Multiple-Hormone Signals in the Modulation of Grape Berry Color Formation. Foods, 2021, 10, 896.	4.3	16
7	The circadian-controlled PIF8â€"BBX28 module regulates petal senescence in rose flowers by governing mitochondrial ROS homeostasis at night. Plant Cell, 2021, 33, 2716-2735.	6.6	48
8	Molecular Evaluation of Kyoho Grape Leaf and Berry Characteristics Influenced by Different NPK Fertilizers. Plants, 2021, 10, 1578.	3.5	4
9	Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine (V. vinifera L.). BMC Plant Biology, 2021, 21, 442.	3.6	4
10	Genome-wide identification and characterization of gibberellin metabolic and signal transduction (GA) Tj ETQq0 0 0 rgBT /Overlock 10 T Biology, 2020, 20, 384.	3.6	10
11	Characterization and temporalâ€"spatial expression analysis of LEC1 gene in the development of seedless berries in grape induced by gibberellin. Plant Growth Regulation, 2020, 90, 585-596.	3.4	5
12	Characterization on the conservation and diversification of miRNA156 gene family from lower to higher plant species based on phylogenetic analysis at the whole genomic level. Functional and Integrative Genomics, 2019, 19, 933-952.	3.5	9
13	VvmiR160s/VvARFs interaction and their spatio-temporal expression/cleavage products during GA-induced grape parthenocarpy. BMC Plant Biology, 2019, 19, 111.	3.6	25
14	Drought stress revealed physiological, biochemical and gene-expressional variations in â€˜Yoshihimeâ€™ peach (<i>Prunus Persica</i> L) cultivar. Journal of Plant Interactions, 2018, 13, 83-90.	2.1	75
15	Characterization of Vv-miR156: Vv-SPL pairs involved in the modulation of grape berry development and ripening. Molecular Genetics and Genomics, 2018, 293, 1333-1354.	2.1	30
16	In silico identification and computational characterization of endogenous small interfering RNAs from diverse grapevine tissues and stages. Genes and Genomics, 2018, 40, 801-817.	1.4	2
17	Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocarpy. Journal of Experimental Botany, 2018, 69, 3639-3650.	4.8	42
18	Abscisic acid, sucrose, and auxin coordinately regulate berry ripening process of the Fujiminori grape. Functional and Integrative Genomics, 2017, 17, 441-457.	3.5	78

#	Article	IF	Citations
19	Characterization of miR061 and its target genes in grapevine responding to exogenous gibberellic acid. Functional and Integrative Genomics, 2017, 17, 537-549.	3.5	12
20	VpPUB24, a novel gene from Chinese grapevine, Vitis pseudoreticulata, targets VpICE1 to enhance cold tolerance. Journal of Experimental Botany, 2017, 68, 2933-2949.	4.8	30
21	RING-H2-type E3 gene VpRH2 from Vitis pseudoreticulata improves resistance to powdery mildew by interacting with VpGRP2A. Journal of Experimental Botany, 2017, 68, 1669-1687.	4.8	32
22	Conservation of microRNA-mediated regulatory networks in response to copper stress in grapevine. Plant Growth Regulation, 2017, 82, 293-304.	3.4	29
23	Overexpression of VpEIFP1 , a novel F-box/Kelch-repeat protein from wild Chinese Vitis pseudoreticulata , confers higher tolerance to powdery mildew by inducing thioredoxin z proteolysis. Plant Science, 2017, 263, 142-155.	3.6	49
24	Characterization of miRNAs responsive to exogenous ethylene in grapevine berries at whole genome level. Functional and Integrative Genomics, 2017, 17, 213-235.	3.5	19
25	Genome-wide identification and characterization of genes involved in carotenoid metabolic in three stages of grapevine fruit development. Scientific Reports, 2017, 7, 4216.	3.3	38
26	Genome-Wide Analysis of the Sucrose Synthase Gene Family in Grape (Vitis vinifera): Structure, Evolution, and Expression Profiles. Genes, 2017, 8, 111.	2.4	56
27	Applications of DNA Technologies in Agriculture. Current Genomics, 2016, 17, 379-386.	1.6	21
28	Fertilization of Grapevine Based on Gene Expression. Plant Genome, 2016, 9, plantgenome2015.09.0083.	2.8	9
29	Characterization of eleven monosomic alien addition lines added from Gossypium anomalum to Gossypium hirsutum using improved GISH and SSR markers. BMC Plant Biology, 2016, 16, 218.	3.6	11
30	Study on Expression Modes and Cleavage Role of miR156b/c/d and its Target Gene Vv-SPL9 During the Whole Growth Stage of Grapevine. Journal of Heredity, 2016, 107, 626-634.	2.4	14
31	Characterization of VvPAL-like promoter from grapevine using transgenic tobacco plants. Functional and Integrative Genomics, 2016, 16, 595-617.	3.5	21
32	Abscisic acid and sucrose regulate tomato and strawberry fruit ripening through the abscisic acidâ€stressâ€ripening transcription factor. Plant Biotechnology Journal, 2016, 14, 2045-2065.	8.3	207
33	Functional Analysis of VvBG1 During Fruit Development and Ripening of Grape. Journal of Plant Growth Regulation, 2016, 35, 987-999.	5.1	16
34	Determination of the precise sequences of computationally predicted miRNAs in Citrus reticulata by miR-RACE and characterization of the related target genes using RLM-RACE. Gene, 2016, 575, 498-505.	2.2	3
35	Discovery of Conservation and Diversification of miR171 Genes by Phylogenetic Analysis based on Global Genomes. Plant Genome, 2015, 8, eplantgenome2014.10.0076.	2.8	64
36	Genomeâ€Wide Mapping and Analysis of Grapevine MicroRNAs and Their Potential Target Genes. Plant Genome, 2015, 8, eplantgenome2014.12.0091.	2.8	35

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37	Characterization of a Calmodulin‐binding Transcription Factor from Strawberry (*Fragaria* ×) Tj ETQq1 1 0.784314 rgBT /Overlock	2.8	18
38	Functional conservation analysis and expression modes of grape anthocyanin synthesis genes responsive to low temperature stress. Gene, 2015, 574, 168-177.	2.2	35
39	RLM-RACE, PPM-RACE, and qRT-PCR: An Integrated Strategy to Accurately Validate miRNA Target Genes. Methods in Molecular Biology, 2015, 1296, 175-186.	0.9	17
40	miR-RACE: An Effective Approach to Accurately Determine the Sequence of Computationally Identified miRNAs. Methods in Molecular Biology, 2015, 1296, 109-118.	0.9	0
41	Transcriptome-wide analysis of dynamic variations in regulation modes of grapevine microRNAs on their target genes during grapevine development. Plant Molecular Biology, 2014, 84, 269-285.	3.9	54
42	Grapevine microRNAs responsive to exogenous gibberellin. BMC Genomics, 2014, 15, 111.	2.8	58
43	Advances in identification and validation of plant <scp>microRNAs</scp> and their target genes. Physiologia Plantarum, 2014, 152, 203-218.	5.2	17
44	Genome-wide identification and analysis of FK506-binding protein gene family in peach (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 40	2.2	6
45	Cloning, expression, and characterization of miR058 and its target PPO during the development of grapevine berry stone. Gene, 2014, 548, 166-173.	2.2	22
46	Depiction of Grapevine Phenology by Gene Expression Information and a Test of its Workability in Guiding Fertilization. Plant Molecular Biology Reporter, 2014, 32, 1070-1084.	1.8	11
47	Computational identification of microRNAs in the strawberry (Fragaria×ananassa) genome sequence and validation of their precise sequences by miR-RACE. Gene, 2014, 536, 151-162.	2.2	18
48	Characterization of target mRNAs for grapevine microRNAs with an integrated strategy of modified RLM-RACE, newly developed PPM-RACE and qPCRs. Journal of Plant Physiology, 2013, 170, 943-957.	3.5	40
49	Computational Identification of MicroRNAs in Strawberry Expressed Sequence Tags and Validation of Their Precise Sequences by miR-RACE. Journal of Heredity, 2012, 103, 268-277.	2.4	38
50	Identification of microRNAs from Amur grape (vitis amurensis Rupr.) by deep sequencing and analysis of microRNA variations with bioinformatics. BMC Genomics, 2012, 13, 122.	2.8	98
51	Characterization of microRNAs Identified in a Table Grapevine Cultivar with Validation of Computationally Predicted Grapevine miRNAs by miR-RACE. PLoS ONE, 2011, 6, e21259.	2.5	47
52	Computational identification of microRNAs in apple expressed sequence tags and validation of their precise sequences by miR‐RACE. Physiologia Plantarum, 2011, 141, 56-70.	5.2	52
53	Deep sequencing of grapevine flower and berry short RNA library for discovery of novel microRNAs and validation of precise sequences of grapevine microRNAs deposited in miRBase. Physiologia Plantarum, 2011, 143, 64-81.	5.2	81
54	Deep sequencing discovery of novel and conserved microRNAs in trifoliate orange (Citrus trifoliata). BMC Genomics, 2010, 11, 431.	2.8	195

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55	MiR-RACE, a New Efficient Approach to Determine the Precise Sequences of Computationally Identified Trifoliate Orange (Poncirus trifoliata) MicroRNAs. PLoS ONE, 2010, 5, e10861.	2.5	55