

# Wenran Wang

## List of Publications by Year in descending order

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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	Abscisic acid and sucrose regulate tomato and strawberry fruit ripening through the abscisic acid stress ripening transcription factor. <i>Plant Biotechnology Journal</i> , 2016, 14, 2045-2065.	8.3	207
2	Deep sequencing discovery of novel and conserved microRNAs in trifoliolate orange ( <i>Citrus trifoliata</i> ). <i>BMC Genomics</i> , 2010, 11, 431.	2.8	195
3	Identification of microRNAs from Amur grape ( <i>Vitis amurensis</i> Rupr.) by deep sequencing and analysis of microRNA variations with bioinformatics. <i>BMC Genomics</i> , 2012, 13, 122.	2.8	98
4	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. <i>Physiologia Plantarum</i> , 2011, 143, 64-81.	5.2	81
5	Abscisic acid, sucrose, and auxin coordinately regulate berry ripening process of the Fujiminori grape. <i>Functional and Integrative Genomics</i> , 2017, 17, 441-457.	3.5	78
6	Drought stress revealed physiological, biochemical and gene-expressional variations in "Yoshihime" peach ( <i>Prunus Persica</i> L) cultivar. <i>Journal of Plant Interactions</i> , 2018, 13, 83-90.	2.1	75
7	Discovery of Conservation and Diversification of miR171 Genes by Phylogenetic Analysis based on Global Genomes. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0076.	2.8	64
8	Grapevine microRNAs responsive to exogenous gibberellin. <i>BMC Genomics</i> , 2014, 15, 111.	2.8	58
9	Genome-Wide Analysis of the Sucrose Synthase Gene Family in Grape ( <i>Vitis vinifera</i> ): Structure, Evolution, and Expression Profiles. <i>Genes</i> , 2017, 8, 111.	2.4	56
10	MiR-RACE, a New Efficient Approach to Determine the Precise Sequences of Computationally Identified Trifoliolate Orange ( <i>Poncirus trifoliata</i> ) MicroRNAs. <i>PLoS ONE</i> , 2010, 5, e10861.	2.5	55
11	Transcriptome-wide analysis of dynamic variations in regulation modes of grapevine microRNAs on their target genes during grapevine development. <i>Plant Molecular Biology</i> , 2014, 84, 269-285.	3.9	54
12	Computational identification of microRNAs in apple expressed sequence tags and validation of their precise sequences by miR-RACE. <i>Physiologia Plantarum</i> , 2011, 141, 56-70.	5.2	52
13	Overexpression of VpEIFP1, a novel F-box/Kelch-repeat protein from wild Chinese <i>Vitis pseudoreticulata</i> , confers higher tolerance to powdery mildew by inducing thioredoxin z proteolysis. <i>Plant Science</i> , 2017, 263, 142-155.	3.6	49
14	The circadian-controlled PIF8-BBX28 module regulates petal senescence in rose flowers by governing mitochondrial ROS homeostasis at night. <i>Plant Cell</i> , 2021, 33, 2716-2735.	6.6	48
15	Characterization of microRNAs Identified in a Table Grapevine Cultivar with Validation of Computationally Predicted Grapevine miRNAs by miR-RACE. <i>PLoS ONE</i> , 2011, 6, e21259.	2.5	47
16	Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocarpy. <i>Journal of Experimental Botany</i> , 2018, 69, 3639-3650.	4.8	42
17	Characterization of target mRNAs for grapevine microRNAs with an integrated strategy of modified RLM-RACE, newly developed PPM-RACE and qPCRs. <i>Journal of Plant Physiology</i> , 2013, 170, 943-957.	3.5	40
18	The role of VvMYBA2r and VvMYBA2w alleles of the MYBA2 locus in the regulation of anthocyanin biosynthesis for molecular breeding of grape ( <i>Vitis</i> spp.) skin coloration. <i>Plant Biotechnology Journal</i> , 2021, 19, 1216-1239.	8.3	39

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19	Computational Identification of MicroRNAs in Strawberry Expressed Sequence Tags and Validation of Their Precise Sequences by miR-RACE. <i>Journal of Heredity</i> , 2012, 103, 268-277.	2.4	38
20	Genome-wide identification and characterization of genes involved in carotenoid metabolic in three stages of grapevine fruit development. <i>Scientific Reports</i> , 2017, 7, 4216.	3.3	38
21	Genome-Wide Mapping and Analysis of Grapevine MicroRNAs and Their Potential Target Genes. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.12.0091.	2.8	35
22	Functional conservation analysis and expression modes of grape anthocyanin synthesis genes responsive to low temperature stress. <i>Gene</i> , 2015, 574, 168-177.	2.2	35
23	RING-H2-type E3 gene VpRH2 from <i>Vitis pseudoreticulata</i> improves resistance to powdery mildew by interacting with VpGRP2A. <i>Journal of Experimental Botany</i> , 2017, 68, 1669-1687.	4.8	32
24	VpPUB24, a novel gene from Chinese grapevine, <i>Vitis pseudoreticulata</i> , targets VpICE1 to enhance cold tolerance. <i>Journal of Experimental Botany</i> , 2017, 68, 2933-2949.	4.8	30
25	Characterization of Vv-miR156: Vv-SPL pairs involved in the modulation of grape berry development and ripening. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1333-1354.	2.1	30
26	Conservation of microRNA-mediated regulatory networks in response to copper stress in grapevine. <i>Plant Growth Regulation</i> , 2017, 82, 293-304.	3.4	29
27	VvmiR160s/VvARFs interaction and their spatio-temporal expression/cleavage products during GA-induced grape parthenocarpy. <i>BMC Plant Biology</i> , 2019, 19, 111.	3.6	25
28	Cloning, expression, and characterization of miR058 and its target PPO during the development of grapevine berry stone. <i>Gene</i> , 2014, 548, 166-173.	2.2	22
29	Applications of DNA Technologies in Agriculture. <i>Current Genomics</i> , 2016, 17, 379-386.	1.6	21
30	Characterization of VvPAL-like promoter from grapevine using transgenic tobacco plants. <i>Functional and Integrative Genomics</i> , 2016, 16, 595-617.	3.5	21
31	Characterization of miRNAs responsive to exogenous ethylene in grapevine berries at whole genome level. <i>Functional and Integrative Genomics</i> , 2017, 17, 213-235.	3.5	19
32	Computational identification of microRNAs in the strawberry ( <i>Fragaria</i> — <i>ananassa</i> ) genome sequence and validation of their precise sequences by miR-RACE. <i>Gene</i> , 2014, 536, 151-162.	2.2	18
33	Characterization of a Calmodulin-binding Transcription Factor from Strawberry ( <i>Fragaria</i> —) Tj ETQq1 1 0,784314 rgBT /Over	2.8	18
34	Advances in identification and validation of plant microRNAs and their target genes. <i>Physiologia Plantarum</i> , 2014, 152, 203-218.	5.2	17
35	RLM-RACE, PPM-RACE, and qRT-PCR: An Integrated Strategy to Accurately Validate miRNA Target Genes. <i>Methods in Molecular Biology</i> , 2015, 1296, 175-186.	0.9	17
36	Flexible Capacitive Pressure Sensor Based on Microstructured Composite Dielectric Layer for Broad Linear Range Pressure Sensing Applications. <i>Micromachines</i> , 2022, 13, 223.	2.9	17

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37	Functional Analysis of VvBG1 During Fruit Development and Ripening of Grape. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 987-999.	5.1	16
38	Characterization and Action Mechanism Analysis of VvmiR156b/c/d-VvSPL9 Module Responding to Multiple-Hormone Signals in the Modulation of Grape Berry Color Formation. <i>Foods</i> , 2021, 10, 896.	4.3	16
39	Study on Expression Modes and Cleavage Role of miR156b/c/d and its Target Gene <i>Vv-SPL9</i> During the Whole Growth Stage of Grapevine. <i>Journal of Heredity</i> , 2016, 107, 626-634.	2.4	14
40	Characterization of miR061 and its target genes in grapevine responding to exogenous gibberellic acid. <i>Functional and Integrative Genomics</i> , 2017, 17, 537-549.	3.5	12
41	Depiction of Grapevine Phenology by Gene Expression Information and a Test of its Workability in Guiding Fertilization. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 1070-1084.	1.8	11
42	Characterization of eleven monosomic alien addition lines added from <i>Gossypium anomalum</i> to <i>Gossypium hirsutum</i> using improved GISH and SSR markers. <i>BMC Plant Biology</i> , 2016, 16, 218.	3.6	11
43	Genome-wide identification and characterization of gibberellin metabolic and signal transduction (GA) Tj ETQq1 1 0.784314 rgBT /Overl Biology, 2020, 20, 384.	3.6	10
44	Fertilization of Grapevine Based on Gene Expression. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0083.	2.8	9
45	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. <i>Functional and Integrative Genomics</i> , 2019, 19, 933-952.	3.5	9
46	Multilayer Flexible Pressure Sensor With High Sensitivity Over Wide Linearity Detection Range (August 2021). <i>IEEE Transactions on Instrumentation and Measurement</i> , 2021, 70, 1-9.	4.7	7
47	Genome-wide identification and analysis of FK506-binding protein gene family in peach ( <i>Prunus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 2.2 6	2.2	6
48	Characterization and temporal-spatial expression analysis of LEC1 gene in the development of seedless berries in grape induced by gibberellin. <i>Plant Growth Regulation</i> , 2020, 90, 585-596.	3.4	5
49	Molecular Evaluation of Kyoho Grape Leaf and Berry Characteristics Influenced by Different NPK Fertilizers. <i>Plants</i> , 2021, 10, 1578.	3.5	4
50	Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine ( <i>V. vinifera</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 442.	3.6	4
51	Genetic and Molecular Regulation Mechanisms in the Formation and Development of Vegetable Fruit Shape. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 1514.	2.5	4
52	Determination of the precise sequences of computationally predicted miRNAs in <i>Citrus reticulata</i> by miR-RACE and characterization of the related target genes using RLM-RACE. <i>Gene</i> , 2016, 575, 498-505.	2.2	3
53	In silico identification and computational characterization of endogenous small interfering RNAs from diverse grapevine tissues and stages. <i>Genes and Genomics</i> , 2018, 40, 801-817.	1.4	2
54	Characterization and regulatory mechanism analysis of VvmiR156a-VvAGL80 pair during grapevine flowering and parthenocarp process induced by gibberellin. <i>Plant Genome</i> , 2022, 15, e20181.	2.8	2

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55	miR-RACE: An Effective Approach to Accurately Determine the Sequence of Computationally Identified miRNAs. <i>Methods in Molecular Biology</i> , 2015, 1296, 109-118.	0.9	0